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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on:
                                                                                                                                                                                                                                                 and is derived
                                                                                                                                                                           Score
 1323
1323
1323
1323
1323
1318
1310
1207
1207
1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                    A_Geneseq_0601:*

| SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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| SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
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| SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                                            is the number of results predicted by chance to have a ater than or equal to the score of the result being printed.
100.0
100.0
100.0
100.0
99.6
99.0
91.2
91.2
90.3
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1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHLIPHWIPLVASLGLLAGG....
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                                                                                                                                                                           Length DB
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                                                                                                                                                                                                                                                 of the total
                                                                                                                                                                           IJ
             AAW76391
AAR36808
AAR32456
AAR32456
AAR32458
AAR36810
AAR36809
AAR36809
AAR36809
AAR36809
 AAR32455
                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ....YLAQQRCNLDDTWEGKIYRV
                                                                                                                                                                                                                                                   score distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search time 45.32 Seconds (without alignments) 337.097 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ltd
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                        Pseudomonas aerugi
Pseudomonas Exotox
PE with inactivate
PE having M1 resid
Full-length PE wit
PE having M1 resid
Full-length PE wit
PE binding/translo
PE binding and tra
                                                                                                                                                               Description
Pseudomonas exc
Ps amino acids
exotox
ids 2-4
 AAW76391
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                                                                                                                                Domain
                                                                                                                                                                           Domain
                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                            Pseudomonas
                                                                                                                                                                                                                                                                                                                                       Exotoxin
                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                             AAW76391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW76391 standard; Protein;
                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                       Α;
                                                                                                                                                                                                                                                                                                                                                                   aeruginosa exotoxin
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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| IL-13 binding chai | AAY95296 | 21 | 380 | 6.7 | 88 |
|--------------------|----------|----|------|------|------|
| Construct containi | AAW56260 | | 359 | ٠ | 88 |
| Mature interleukin | AAW56261 | | 315 | 6.7 | 88 |
| Peptide related to | AAP82349 | | 16 | ٠ | 91 |
| acid | AAW46771 | | | • | ω |
| acid seque | AAW46761 | 19 | 1684 | | 93.5 |
| prote | AAW25671 | 18 | 1684 | | 93.5 |
| sequen | AAB07463 | 21 | 25 | ٠ | 128 |
| A chimeric toxin c | AAY43545 | 20 | 635 | 9 | 1181 |
| 3 | AAY43547 | 20 | 634 | 89.3 | 1181 |
| Pseudomonas exotox | AAR40112 | 14 | 613 | 9 | 1187 |
| | AAR40109 | 14 | 613 | œ. | 1187 |
| | AAR40104 | 14 | 613 | 9 | 1187 |
| Pseudomonas exotox | AAR40111 | 14 | 613 | œ. | 1190 |
| Pseudomonas exotox | AAR40110 | 14 | 613 | 9 | 1190 |
| | AAR40108 | 14 | 613 | œ. | 1190 |
| Pseudomonas exotox | AAR40107 | 14 | 613 | 9 | 1190 |
| S | AAR40106 | 14 | 613 | 9 | 1190 |
| eudomonās ex | AAR40105 | 14 | 613 | 9 | 1190 |
| binding | AAR32469 | 14 | 917 | 0 | 1195 |
| ` | AAR36821 | 14 | 917 | 0 | 1195 |
| н | AAR32468 | 14 | 670 | 0. | 1195 |
| PE-Influenza A vir | AAR36820 | 14 | 670 | 0 | 1195 |
| \mathbf{r} | AAR32453 | 14 | 665 | 0 | 1195 |
| Pseudomonas exotox | AAR36805 | 14 | 665 | 0 | 1195 |
| ⊂ | AAR87738 | 16 | 614 | 0 | 1195 |
| seque | AAB07462 | 21 | 613 | 0 | 1195 |
| sp. | AAW92912 | 20 | 613 | 0 | 1195 |
| sp. e | AAW92915 | 20 | ₩ | 0 | 1195 |
| aerug | AAW59278 | 19 | | 0 | 1195 |
| | AAR40113 | 14 | 613 | 0 | 1195 |
| 0 | AAR40102 | 14 | ₩. | | 1195 |
| (2-414)-Ma(57-6 | 24 | 14 | 426 | | 1195 |
| PE domains I and I | AAR36806 | 14 | 426 | 90.3 | 1195 |

ALIGNMENTS

638

A

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01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                   aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ETA; toxA gene; drug delivery; membrane transport.
                                                                                                           /note= "enzymatic ADP-ribosylation domain"
634..638
                                                                                                                                                    405..613
/label= III
                                                                                                                                                                                                                            /note= "membrane 365..404
                                                                                                                                                                                                                                                                                 /note= "receptor binding domain"
253..364
                                                                                                                                                                                    /label= I
/note= "receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           /Label=
                                                                                                                                                                                                                                                                    'label= II
                                                                       "peptide important for intracellular
transport and cytotoxicity of ETA"
                                                                                                                                                                                                                                              penetrating domain"
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24-MAR-1998; 26-MAR-1997;

(TEXA) UNIV TEXAS

SYSTEM

97US-0042056 98WO-US05710

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RESULT
AAR36808
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                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exotoxin A (ETA), a virulence factor and secreted protein encoded CC by the toxA gene (see AAV61784). The invention employs a group of CC membrane penetrating proteins, of which ETA is an example, to CC carry a variety of therapeutic agents across the cellular membrane CC carry a variety of therapeutic agents across the cellular membrane CC card, peptide, peptide nucleic acid, (single chain) antibody, or CC control of a eukaryotic promoter (e.g. the cytomegalovirus control of a eukaryotic promoter (e.g. the cytomegalovirus control of a eukaryotic promoter (e.g. the cytomegalovirus conding protein, single chain antibody, tumour suppressor, it CC cytokine, hormone, toxin, or is an oncogene. Alternatively, it CC cytokine, hormone, toxin, or is an oncogene. Alternatively, it CC cytokine, hormone toxin, or is an oncogene or viral CC cytokine, and itsense molecule that targets an oncogene or viral CC cytokine, and its ability to transport molecules across membranes, or CC transing its ability to transport molecules across membranes, or CC cytokine, and protein of a free cysteine in domain III (see AAW61787). CC conjugates of ETA, specifically peptide nucleic acids (see AAW61787). CC conjugates of ETA, specifically peptide nucleic acids (see AAW61787). CC chain istered, thereby reducing toxicity, and provide effective cargetting of an agent to a specific point within a cell.
                                                                                                                                    δÃ
                                                                                                                                                                      В
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AC X
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Best Local S
Matches 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delivering compounds to cells as new conjugate with detoxified exotoxin A - able to cross membranes and deliver to the cytoplie.g. nucleic acids, antibodies, tumour suppressors etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV61784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-532023/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 58-60; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
 AAR36808;
                               AAR36808 standard;
                                                                                                           241
                                                                                                                                        241
                                                                                                                                                                         181
                                                                                                                                                                                                       181
                                                                                                                                                                                                                                      121
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                                                                                                                                         LDDTWEGKIYRV 252
                                                                                                           lddtwegkiyrv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                             252
                               Protein; 652
                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1323; DB 19; 100.0%; Pred. No. 2.2e-129; tive 0; Mismatches 0;
                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytoplasm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                638;
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240 180 60 60

0

0;

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δÃ
                                                                                                              Вb
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                                                                                                                                                                   Qy
Дb
                Qy
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                                                                        DЬ
                                                                                                                                                                                        Matches
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                              Plasmid pVCPE/2 was made by replacing the 105bp PpuMI/EcoRI fragment of pVC45DF+T (containing the Pseudomonas Exotoxin coding region) with a 46bp DNA fragment (AAQ41718) encoding an in-frame duplication of PE codons 604 to 613 flanked by unique restriction sites. This construct is used for generating full-length molecules of PE with the deletion of residue 553 resulting in an inactivated toxin domain (AAQ41719) fused to chosen protein segments between
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-154266/19.
N-PSDB; AAQ41719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP541335-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP-ribosylating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA encoding bacterial toxin-antigen conjugates useful as vaccines against viral infections, tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                           Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Donnelly JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-1993
                                                                                                                                                                                                                                                                                                                                        Example 7; Page 34-37;
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                        PE codons
                 241
                                     181
                                                                         121
                                                                                            121
241
                                                       181
                                                                                                              61
                                                                                                                                 61
                                                                                                                                                                                                 Local Similarity
                                                                                                                                                 lddtwegkiyrv
                  LDDTWEGKIYRV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; Ma; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytotoxic T lymphocyte; CTL; influenza A virus; rotein; Ma; cell recognition domain; translocati sylating domain; anti-viral agent.
                                                                                                                                                                                                                                                        604 and 605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exotoxin with inactivated toxin
                                                                                                                                                                                                                                      652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                       100.0%; Score 1323; DB 14; ilarity 100.0%; Pred. No. 2.3e-129; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        & CO
                                                                                                                                                                                                                                                                                                                                                                                                                             Friedman A,
, Oliff AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0792507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92EP-0310067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
 252
                                                                                                                                                                                                                                                                                                                                           81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             Hawe LA, Liu
Shi X, Ulmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ť
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nonsense codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Marshall MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain;
                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                  are
                                                                                                                                                                                             Gaps
                                                           240
                                                                                                180
                                                                                                                                     120
                                                                              180
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swslnwlvpighekpsnikvfihelnagnqlshmspiytiemgdellaklardatffvra 180
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                                                                                    LDDTWEGKIYRV 252
                                                                                                     WPI; 1993-087107/11.
                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              668 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR32457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Donnelly JJ, F
Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERI ) MERCK
                                                                                                                                                                                                                                              20-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP532090-A.
                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                  AAR32457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 7 describes the construction of pVCPE/2 (pVC45DF+T/2).

pVCPE/2 was made by replacing the 105 base pair PpuMI/ECORI
fragment of pVC45DF+T with a 46 base pair DNA fragment encoding an
inframe duplication of recodons 604 to 613 flanked by unique cloning
sites. This construct is used for generating full-length mols. of PE
with the deletion of residue 553 resulting in an activated toxin
domain (AAQ36019) fused to protein segments of choice between PE
codons 604 and 605. One may replace the ompA signal sequence
with the promoter/ribosome binding site as described for pVC-PEMI-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWSLMWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MHLIPHWIPLVASLGLLAGGSSASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA 60
                                                                                                                                                                                                                                                                                     /note- "residue not defined in the specification; encoded by stop codon TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
                                                                                                                                                         PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; flusion; hybrid; pvC45DF.72; pvC45DF.47.2; pvC-PEM1-2; duplication; ompa; signal sequence; promoter; ribosome binding site; RBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marshall MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MA,
J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LA, Liul
X, Ulmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; Page 78 + 37-40; 85pp; English.
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hawe LA,
Shi X,
                                         AAR32456 standard; Protein; 652 AA.
                                                                                                                              PE with inactivated toxin domain.
                                                                                                                                                                                                                                                                                                                                                                                       92EP-0202660
                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0756249
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friedman A,
, Oliff AI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1993-087107/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-087107,
N-PSDB; AAQ36019
                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Donnelly JJ, F;
Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                       02-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-1991;
                                                                                                  20-JUL-1993
                                                                                                                                                                                                                                                                                                                                                            17-MAR-1993.
                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                      AAR32456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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Example 8 describes the construction of pVCPE/2-Ma. pVCPE/2-Ma was made by ligating into the XmaI site of pVCPE/2 a 48 base pair DNA fragment encoding amino acids 55 through 67 (AAQ36020). This construct expresses in E.coli full-length PE with MI amino acids 55 through 67 inserted between PE amino acids 604 and 605 (AAQ38394). One may replace the ompA signal sequence with the promoter/ribosome binding site as described for pVC-PEMI-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MHLIPHWIPLVASLGLLAGGSSASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA 60
/note- "residue not defined in the specification;
encoded by stop codon TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               having M1 residues 55 through 67 between residues 604 and 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion; hybrid; pVCPE/2-Ma; pVC-PEM1-2; ompA; signal sequence; promoter; ribosome binding site; RBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marshall MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacterial toxin-antigen protein conjugates - to elicit (
T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1323; DB 14; 100.0%; Pred. No. 2.3e-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Liu MA,
Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 40-42; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hawe LA,
Shi X, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 ¥
                                                                                                                                                                                                                                                                                                              AAR32457 standard; Protein; 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0756249.
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Oliff AI,
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                                                                                                         240
            180
DINGOGVLHYSMYLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pVCPE/1-MI:15-106 was made by subcloning a PCR-amplified DNA fragment encoding MI amino acids 15 to 106 into the XmaI site of pVCPE/2 (see AAQ41718). The primers used in the amplification reaction had sequences AAQ41722 and AAQ41723. The construct express in E.coli full-length PE with MI amino acids 15-106 inserted between PE amino acid 604 and 605 (see AAQ41724).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful as vaccines against viral infections, tumours and parasites
                                           SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA
                                                    181 HESNEMQPTLAISHAGVSVVMAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN
                                                                                               PE with Influenza A virus MI codons 15-106 inserted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marshall MS;
                                                                                                                                                                                                                                                                                             influenza A virus;
                                                                                                                                                                                                                                                                                            Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus
matrix protein; anti-viral agent; Pseudomonas exotoxin.
                                                                                                                                                                                                                                                                                                                                                                        744
/note= "corresponds to nonsense codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Liu MA,
Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 9; Page 45-47; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hawe LA,
Shi X, U
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                         AAR36810 standard; Protein; 746 AA
                                                                                                                                                                                                                                                                                                                              Chimeric Pseudomonas aeruginosa.
Chimeric Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 92EP-0310067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0792507
                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Friedman A,
Oliff AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MERI ) MERCK & CO INC.
                                                                                                                                 241 LDDTWEGKIYRV 252
                                                                                                                                             241 lddtwegkiyrv 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-154266/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ41724
                                                                                                                                                                                                                                                                                                                                                                Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Donnelly JJ, F.
Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      746
                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1992;
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                                                                                                                                                                                                                                                      25-AUG-1993
                                                                                                                                                                                                                                                                           Full-length
                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                        EP541335-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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      61
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Gaps

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Indels

100.0%; Score 1323; DB 14; 1larity 100.0%; Pred. No. 2.8e-129; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 252; Conserv

Length 746;

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Example 9 describes the construction of pVCPE/2-M1:15-106. pVCPE/2-M1:15-106 was made by subcloning a PCR-amplified DNA fragment encoding M1 amino acids 15 through 106 into the Xmal site of pVCPE/2. The sequence of the oligonucleotide primers used to amplify the M1 segment are those shown in AAQ38395-96, respectively. This construct expresses in E.coli full length PE with M1 amino acids 15 through 106 inserted between PE amino acids 604 and 605 (AAQ38397).
                                                                                                                                                                          180
                                                                                                                       240
                                                     120
                                                                               120
                         9
                                                                                                                                                                                                                                                                                                                                                                                                                          PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion; hybrid; pVCPE/2-M1:15-106; pVCPE/2; ompA; signal sequence; promoter; ribosome binding site; RBS; primer; PCR; amplification.
MHLIPHWIPLVASLGLLAGGSSASAABEBAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA
                                                     DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG
                                                                   SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA
                                                                                                                                                               181 HESNEMQPTLAISHAGVSVVMAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN
                                                                                                                                                                                                                                                                                                                                                                                               PE having M1 residues 15 through 106 between residues 604 and 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "residue not defined in the specification;
encoded by stop codon TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marshall MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial toxin-antigen protein conjugates - to elicit in T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   МА,
ц,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Liu l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 48-50; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hawe LA,
Shi X, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
744
                                                                                                                                                                                                                                                                                                                    AAR32458 standard; Protein; 746 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92EP-0202660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-0756249.
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Friedman A,
, Oliff AI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                           241 LDDTWEGKIYRV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-087107/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ38397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Donnelly JJ, F
Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                            20-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP532090-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                 AAR32458;
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RESULT
AAR36
AAR36
AAR36
AC AAR3
AC AAR3
AC Full
AC AAR3
AC Full
AC AAR3
AC AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                      useful as
parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; cytotoxic T lymphocyte; CTL; influer matrix protein; Ma; cell recognition domain; ADP-ribosylating domain; anti-viral agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR36809 standard; Protein; 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One may replace the ompA signal sequence with the promoter/ribosome binding site as described for pVC-PEM1-2.
                                                                                                                                                                                                                                                                           08-NOV-1991;
                                                                                                                                                                                                                                                                                                                 04-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Full-length PE with Influenza virus MI fragment inserted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR36809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric
  Example 8; Page 36-42; 81pp; English
                                                        Recombinant DNA encoding bacterial toxin-antigen conjugates useful as vaccines against viral infections, tumours and
                                                                                                                     N-PSDB; AAQ41721.
                                                                                                                                                                          Donnelly JJ,
Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                        12-MAY-1993
                                                                                                                                                                                                                                    (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDDTWEGKIYRV 252
|||||||||||
||1ddtwegkiyrv 252
                                                                                                                                     1993-154266/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HESNEMOPTLAISHAGVSVVMAQTOPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
Influenza A Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                            Friedman A,
                                                                                                                                                                                                                                                                           91US-0792507
                                                                                                                                                                                                                                                                                                                 92EP-0310067
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 666
                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "corresponds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%;
                                                                                                                                                                            Hawe
Shi x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1318; DB 14; Pred. No. 9.2e-129;
                                                                                                                                                                            x, Ulmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      influenza A virus;
domain; translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                     nonsense codon'
                                                                                                                                                                            , F
W
W, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                              Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain;
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                                                                              are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ωy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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AAR36822
ID AAR3
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 251; Conserv
                                                                                                                                                                                                                                    Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pVCPE/2-Ma was made by ligating into the XmaI site of pVCPE/2 (see AAQ41718) a 48bp DNA fragment encoding amino acids 67 of Influenza A virus. The resulting construct expresses in E. full-length PE with MI amino acids 55-67 inserted between PE amiacid 604 and 605 (see AAQ41721).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                    WPI; 1993-154266/19.
N-PSDB; AAQ41731.
                                                                                                  Donnelly JJ,
Montgomery DI
                                                                                                                                                                                                                                                                                                                                                           AAR36822 standard;
                            parasites
                                     Recombinant DNA encoding bacterial toxin-antigen conjugates useful as vaccines against viral infections, tumours and
                                                                                                                                                    08-NOV-1991;
                                                                                                                                                                        04-NOV-1992;
                                                                                                                                                                                             12-MAY-1993
                                                                                                                                                                                                                                                                   AIDS;
                                                                                                                                                                                                                                                                            Vaccine;
                                                                                                                                                                                                                                                                                               PE binding/translocation domains-HIV gag fusion protein
                                                                                                                                                                                                                                                                                                                   25-AUG-1993 (first entry)
                                                                                                                                (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                              241
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                                                                                                                                                                                                                                                                                                                                                                                                            | LDDTWEGKIYRV :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dtngqgvlhysmvleggndalklaidnalsitsdgltirleggvepnkpvrysytrqarg
                                                                                                                                                                                                                                                                 ne; cytotoxic T lymphocyte; CTL; Human Immunodeficiency Virus; anti-viral agent; Pseudomonas exotoxin; fusion construct.
                                                                                                                                                                                                                                   Human Immunodeficiency Virus. Pseudomonas aeruginosa.
                                                                                                  DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       668 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                  Friedman A,
,, Oliff AA,
                                                                                                                                                     91US-0792507
                                                                                                                                                                         92EP-0310067
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                                                                                                                                                                                                                                                                                                                                                            Protein;
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       81pp;
                                                                                                  Hawe LA,
Shi x, U
                                                                                                                                                                                                                                                                                                                                                            937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1310; DB 14;
Pred. No. 5.3e-128;
0; Mismatches 1;
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                                                                                                  Ulmer
                                                                                                  Ţ;Ķ
                                                                                                            Marshall MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Example

26; Page 70-74;

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ARRESULT

ARABAZIATO

ARABAZIATO

XX ARABAZIATO

AC AARABAZIATO

AC AARABAZIAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A fragment containing the HIV gag gene was obtained from plasmid HIVPBR322 by PCR with primers that added a SacII site adjacent to the ATG codon of gag (to give the sequence AAQ41729), and a SacI immediately after the termination codon at the 3' end (to give the sequence AAQ41730). The PCR fragment was cloned into plasmid pvC45DF+7 (containing Pseudomonas Exotoxin sequence). In the resulting plasmid, pVC-ompA-PEGAG, the binding and translocation domains of PE were fused to the gag gene of HIV-1. The fusion contains an own leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contains
Bacterial toxin-antigen protein conjugates - to elicit T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion; hybrid; pVC-ompA-PEGAG; HIV-1; HIVpBR322; pVC45DF+T; PCR; amplification; binding; translocation; domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PE binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR32470 standard; Protein; 937
                                                                                                                                                                                         Montgomery DL,
                                                                                                                                                                                                               Donnelly JJ,
                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                            09-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                          02-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                      17-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP532090-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rv 251
                                                                                                                                               1993-087107/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                         AAQ38414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an ompå leader.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                           Friedman A,
, Oliff AI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translocation domains -
                                                                                                                                                                                                                                                                                                              91US-0756249.
                                                                                                                                                                                                                                                                                                                                                          92EP-0202660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.2%;
95.5%;
                                                                                                                                                                                           Hawe LA,
Shi X, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1207; DB 14; Pred. No. 5e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                              A, Liu
Ulmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV GAG fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                      Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
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RESULT 10
AAR36807
ID AAR368
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The HIV GAG gene was obtained from plasmid HIVpBR322 by
CC Pick with oligonucleotide primers which added a SacII site
CC adjacent to the ATG codon of GAG to give the sequence of
CC AAQ38412, and a SacI site immediately after the termination
CC codon at the 3' end to give the sequence shown in AAQ38413.

CC rhe PCR fragment was digested with SacII and ligated to the
CC plasmid pvC45DP+T, which had been digested with EcoRI, the 5',
CC overhang filled in by Klenow fragment, and digested with SacII.
CC overhang filled in by Klenow fragment, and digested with SacII.
CC overhang filled in by Klenow fragment, and digested with SacII.
CC construction fuses the binding and translocation domains of PE
CC construction fuses the binding and translocation domains of PE
CC compA leader sequence. Alternatively, any vector contg. the complete
CC coding region for HIV GAG can be used with these oligomers to generate
CC the HIV GAG gene by HIV.
                                                                                                                                                                                                                                                                                                                                                                                   밁
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Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 73-77; 85pp; English
                                                                                                                                              Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; matrix protein; Ma; Pseudomonas exotoxin; cell recognititranslocation domain; anti-viral agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                         25-AUG-1993 (first entry)
                                                                                                                                                                                                                                                                       AAR36807 standard; Protein; 414 AA.
                        08-NOV-1991;
                                                04-NOV-1992;
                                                                                                                      Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                     130
                                                                       12-MAY-1993.
                                                                                                                                                                                                                                                                                                                                                                                  131
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| 250 rv 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                937 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                exotoxin domains I and II encoded by pVC-PEBT
                          91US-0792507
                                                 92EP-0310067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1207; DB 1
Pred. No. 5e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14;
                                                                                                                                                                cell recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              937;
                                                                                                                                                                 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190
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(MERI) MERCK

& CO INC

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RESULT 11
AAR324
XX AAR324
XX AAR324
AC AAR324
XX PE; Ps
KW T7 poll
XX FT poll
XX Synthe
XX EP532C
XX EP532C
XX O2-SEI
XX O2-SEI
XX Donnel
PI Montg
XX WPI;
DR WPI;
DR WPI;
DR WPI;
DR WPSD
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful as
parasites
                                                                                                                                                                                                     PE amino acids 2-414.
                                                                                                                                                                                                                                                           AAR32455 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Control plasmid pVC-PEBT encodes a T7 promoter-driven gene is consisting of PE amino acids 2-414 followed by termination (instead of by at least part of the influenza A virus Matrix protein (as in e.g. AAQ41714).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 30-32; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA encoding bacterial toxin-antigen conjugates useful as vaccines against viral infections, tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Donnelly JJ, |
Montgomery DL,
                                                                                                  02-SEP-1992;
                                                                                                                                                                                                                        20-JUL-1993
           N-PSDB; AAQ37108
                                                                                 09-SEP-1991;
                   WPI; 1993-087107/11
                                    Donnelly JJ,
Montgomery DL,
                                                              (MERI ) MERCK
                                                                                                                                                                                                                                                                                                         182
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                                                                                                                                                                           polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1993-154266/19.
DB; AAQ41715.
                                                                                                                                                                                                                                                                                                      AEEAFDLWNECAKACYLDLKDGVRSSRMSVDPAIADTNGGGVLHYSMYLEGGNDALKLAI 85
                                                                                                                                                                                                                                                                                                                                                                                                                  aeeafdlwnecakacvldlkdgvrssrmsvdpaiadtngqgvlhysmvleggndalklai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Friedman A, Oliff AA,
                                    Friedman A,
, Oliff AI,
                                                              & CO INC
                                                                                 91US-0756249
                                                                                                  92EP-0202660
                                                                                                                                                                           fusion;
                                                                                                                                                                        exotoxin; influenza A virus; M1; matrix protein;
fusion; hybrid; pvC-PEBT; pvC-PEM1-2.
                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.3%;
                                   Hawe LA,
Shi x, (
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Shi X, U
                                                                                                                                                                                                                                                            414
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1195; DB 14;
Pred. No. 2.7e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                    Ulmer J;
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                                              Marshall
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                                              SM
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Best Local S
Matches 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human
                                                                                                                                                                                                       Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; matrix protein; Ma; Pseudomonas exotoxin; cell recognition translocation domain; anti-viral agent; fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 33-35;
                                                                                                                                                                                   Chimeric Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                    08-NOV-1991;
                                        04-NOV-1992;
                                                                                                                        Region
                                                                                                                                           Region
                                                                                                                                                                           Chimeric
                                                                                                                                                                                                                                                                                                               AAR36806 standard;
                                                                                EP541335-A.
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                                                                                                                                                                                                                                                 domains I and II fused to influenza A virus
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                                                                                                                                                                                                                                                                                                                                                              AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity
227; Conserv
                                                                                                                                                                           Influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                      (first entry)
                    91US-0792507
                                        92EP-0310067
                                                                                                                       /note= "PE domains I
415..426
                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.3%;
                                                                                                  "amino acids 57-68
Matrix protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1195; DB 14;
Pred. No. 2.7e-116;
0; Mismatches 0;
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                                                                                                              of.
                                                                                                              Influenza
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                                                                                                              A Virus
                                                                                                                                                                                                                    domain;
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(MERI) MERCK & CO INC

Donnelly JJ, Montgomery DL,

Friedman A,
 Oliff AA,

Hawe LA, Shi X, (

, Liu Ulmer ΜA,

Marshall

MS

WPI; 1993-154266/19

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RRESULT 1
AAR32454
ID AAR3
XX AAR3
AC AAR3
XX PE;
DE PE(;
XX PE;
XX OMPA
KW OMPA
KW OMPA
KW Inii
XX PYC
XX Syni
XX Syni
XX EP5
PN EP5-
XX X PF 02--
XX (ME)
PA (ME)
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An MI gene fragment (encoding amino acids 57-68 of influenza A virus matrix protein) was subcloned into BS-PE, a plasmid constructed by inserting a 1.3kb NruI/SacII fragment of plasmid pVC45-PFT containing the domain I and II coding regions of Pseudomonas exotoxin into pBluescript II SK restricted with HincII and SacII. The PE-derived portion of the hybrid protein allows internalisation of the protein by an antigen-presenting cell. The hybrid protein is then processed and an antigenic segment (i.e. the Influenza A virus matrix protein) is presented on the cell surface where it elicits an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant DNA encoding bacterial toxin-antigen conjugates useful as vaccines against viral infections, tumours and
                                                                                                                                                                  PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; ompA; leader; signal; fusion; hybrid; BS-PEMa-1; pVC45DR+T; pVC-PEMa-1; T7 promoter; RBS; ribosome binding site;
                                                                                                                                                                                                                                                                                                AAR32454 standard;
                           09-SEP-1991;
                                                    02-SEP-1992;
                                                                              17-MAR-1993.
                                                                                                                              Synthetic
                                                                                                                                                                                                                      PE(2-414)-Ma(57-68) hybrid
                                                                                                                                                                                                                                             20-JUL-1993
                                                                                                                                                         initiation
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                                                                                                                                                                                                                                                                                                                                                            {\tt nagnqlshmspiytiemgdellaklardatffvrahesnemqptlaishagvsvvmaqtq}
                                                                                                                                                                                                                                                                                                                                                                                                                           NAGNOLSHMSDIYTIEMGDELLAKLARDATFFVRAHESNEMOPTLAISHAGVSVVMAQTQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
    MERCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 AA;
                                                                                                                                                      sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.3%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                              (first entry)
                            91US-0756249
                                                    92EP-0202660
    င္ပ
                                                                                                                                                                                                                                                                                                Protein; 426
    INC
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                                                                                                                                                         build-back
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                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1195; DB 14;
Pred. No. 2.8e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acids 57-68 of influenza A virus
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                                                                                                                                                                                                                                                                                                   AA.
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                                                                                                                                                                                   matrix protein;
pVC45DR+T;
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RESULT 1
AAR40102
ID AAR4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-lymphocyte immune response, used for preventing viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                    steric
                                                             target site; cytotoxin; unpaired cysteine; monoclonal antibody; ligand; cell surface;
                                                                                                                 Pseudomonas exotoxin for site-specific mutation with unpaired
                                                                                                                                             27-JAN-1994
                                                                                                                                                                                                 AAR40102 standard; Protein;
                         Pseudomonas
                                                                                         Pseudomonas exotoxin; PE; diphtheria toxin;
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les 227; Conserv
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                                                                                                                                                                                                                                                              NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ
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                                                                                                                                                                                                                                                                                                                                                                      \tt dnalsits dgltirleggvepnkpvrysytrq argswslnwlvpighekpsnikvfihel
                                                    unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                          aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Friedman A,
                                                                                                                                               (first entry)
                                                    cysteine;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.3%;
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                                                     s.u.c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1195; DB 14;
Pred. No. 2.8e-116;
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Ulmer
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                                                                   receptor; binding
mutation;
                                                                                              DT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marshall MS;
                                                                                              immunotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                  site;
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Query Match
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Matches 227
                                                                                                                                                                                                                                                                                              or near the cytotoxin's receptor-binding site, and retains the same receptor-binding ability and cytotoxicity as the native cytotoxins provided they are not conjugated with a binding mol. The toxins are cross-linked through the free SH group of their unpaired cysteine residues to binding mols. (including monoclonal antibodles, fragments and other ligands) to form immunotoxins, and these immunotoxins do not bind to the cell surface receptors which are bound by the native cytotoxin. However, when the cross-linker is cleaved and the binding mol. is released, the cytotoxin regains
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 20-23; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Site-specifically mutated cytotoxin(s) with an unpaired cysteine - such that conjugation of a binding mol. to the Cys blocks receptor binding used as immuno:toxins for highly specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-258616/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-1993;
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Misc-difference 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The new mutated toxin has an unpaired cysteine residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TANO-) TANOX
   121
                               146
                                                                                                                                                                                              Local Similarity
                                                            5
                                                                                        98
                                                                                                                                                 26
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                                                                                                                                                                                                                                                                                   receptor-binding ability and its cytotoxicity
                                                                                                                  NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ 205
                                                          DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
                                                                                                                                                                                                                                                        613 AA;
                                                                                                                                                                               Conservative
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- 25
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182
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188
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158
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245
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223
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                                                                                                                                                                                             Score 1195; DB 14;
Pred. No. 4.8e-116;
                                                                                                                                                                               Mismatches
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Matches 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Site-specifically mutated cytotoxin(s) with an unpaired cysteine - such that conjugation of a binding mol. to the Cys blocks receptor binding used as immuno:toxins for highly specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   target site; cytotoxin; unpaired cysteine; monoclonal antibody; ligand; cell surface; steric unpaired cysteine; s.u.c.
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                                                                                                   DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
dnalsitsdgltirleggvepnkpvrysytrqargswslnwlvpighekpsnikvfihel
                                                                                                                                                                                                                Similarity 100
27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 20-23; 30pp; English.
                                                                                                                                                                                                                                                                                                                                               613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Pred. No. 4.8e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1323
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US-08-255-0246-1
US-09-046-992-2
US-08-665-259-25
US-08-762-500-75
US-08-762-500-75
US-08-846-340-4
US-08-846-340-4
US-08-846-340-3
US-08-846-340-3
US-08-846-340-3
US-08-846-348-26
US-08-846-348-26
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US-08-846-348-26
US-08-846-348-26
US-08-4465-6
US-08-284-465-6
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US-08-284-465-6
US-08-334-34-28
US-09-687-594-28
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US-08-405-615-1
US-08-461-234-1
US-08-463-480-1
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| RESULT 1 US-09-047-148- Sequence 2, Sequence 2, Patent No. 6 GENERAL INF APPLICANT TITLE OF TITLE OF TITLE OF NUMBER OF NUMBER OF CORRESPON CORRESPON STREET: CITY: | | 45 | 43 | 42 | 40 41 | 39 | 38 | 36 37 | 35 | 3 (4. | ω ω () | ω | 30 | 29 | 28 |
|--|------------|--|------------------|-------------------|------------------|------------------|-------------------|-----------------|------------------|--------------------|--------------------|-----------|-----------|--------|-------------------|
| O9-047-148-2 09-047-148-2 09-047-148-2 equence 2, Application atent No. 6086900 GENERAL INFORMATION: APPLICANT: Draper, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: OF SEQUENCES: CORRESPONDENCE ADDRE ADDRESSEE: ATOOLG STREET: P.O. BOX CITY: Houston | | 73.5 | 73.5 | ω. | 73 5 | 74 | 74 | 74.5 | | 74.5 | 74.5 | 7 | 76 | 76.5 | 76.5 |
| -2 Application US/09047148 5086900 FORMATION: FORMATION | | 5. 6 | | 5.6 | | | | л (л n (л | | | | | | 5.8 | 5. 80 |
| 10.E: 5 | | 352 | 224 | 224 | 225 | 435 | 337 | 2647 | 2647 | 551 | 550 | 1794 | 1489 | 599 | 349 |
|)90, for HOD: HOD: MI | | <u>ب</u> | п 4 | N 1 | - 4 | 4 | 4 | > N | N | ν, | s N | 6 | 6 | 4 | ω |
| US/09047148 ockford methods and compositions for USING methods and compositions for USING CELL MEMBRANES 13 S: White & Durkee | ALIGNMENTS | US-07-923-260A-6 | US-08-849-764C-2 | US-09-111-070-2 | US-09-066-047-13 | US-09-066-046-27 | US-08-871-572B-4 | US-08-779-113-8 | US-08-583-562B-8 | US-08-417-210A-143 | US-08-417-210A-140 | 5183745-6 | 5183745-2 | -145-2 | US-08-970-428A-14 |
| JSING TO CARRY MATERIALS ACROSS | | Sequence 2, Appli Sequence 6, Appli | กัก | Sequence 2, Appli | 2 13 | 27 | Sequence 1, Appli | , @ | | Sequence 143, App | 140, | • | • | N | Sequence 14, Appl |

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US-09-047-148-2
Query Match
Best Local Similarity
Matches 252; Conserv
                                                                                                                                                                                                                                                    CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/042,056

FILING DATE: 26-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: UTSF:072

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 18-3000
                                                                                                                                                                            TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 638 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Arnormal CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                         TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UI
ZIP: 77210
                                                                                                                       TOPOLOGY:
  100.0%; Score 1323; DB 3; ilarity 100.0%; Pred. No. 3e-137; Conservative 0; Mismatches 0;
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                                                                                                                         linear
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    Indels
                                       Length
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    0;
    Gaps
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61 61

DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG DTNGQGYLHYSMYLEGGNDALKLAIDNALSITSDGLTIRLEGGYEPNKFVRYSYTRQARG

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US-08-405-615-1
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                                                        Matches 227;
                                                                         Best Local Similarity
                                                                                     Query Match
                                                                                                                                                                                                                                      TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with TITLE OF INVENTION: Increased Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pastan, ira APPLICANT: FitzGerald, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 613 amino acids
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                           NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWSLNWLVPIGHERPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA 180
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                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08405615
                                                                                                                                               TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Ellen L. Weber
One Market Plaza, Steuart Tower, Suite
                                                                                                                                                                                                                                                   415-543-5043
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                                                           Conservative
                                                                                                                                                             ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                       90.3%;
                                                                                                                                                                                                                                                                                                                                                                   us/07/901,709
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                                                                                                                                                                                                                                                                                                          32,762
                                                           0;
                                                                                                                                                                                                                                                                                                15280-36
                                                           Score 1195; DB 1;
Pred. No. 3.8e-123;
0; Mismatches 0;
                                                                                      Length 613;
                                                              Indels
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                                                              Gaps
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US-08-461-234-1
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                                                                                            Query Match
Best Local :
                                                                               Matches
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                                                                                                                                                                                                                                                             TELEFAX: (415) 543-50 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PATENTIN Rel-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 05-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                  APPLICATION 15-MAR INTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT, Ellen Lauver
32,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                               MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 613 amino acids
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 NAGNQLSHMSDIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US UFFILING DATE: 18-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 15-MAR-1995
                                                                             Local Similarity es 227; Conserv
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86
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DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
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                                                                                                                                                                                                                       amino acid
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                        (415)
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                                                                                                                                                                                                                                                                           543-5043
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ald, David J.
                                                                                                                                                                                                                                                                                         543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increased Activity
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                                                                                                                                                                                                                                                                                                                     15280-36-3
                                                                                 0;
                                                                                              Score 1195; DB 2; pred. No. 3.8e-123;
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #1.30
                                                                                    0;
                                                                                                             Length 613;
                                                                                    Indels
                                                                                    0;
                                                                                    Gaps
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US-08-463-480-1
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                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/405,615
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-36-2
REFERENCE/DOCKET NUMBER: 15280-36-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08463480 Patent No. 5854044
                                                                                                                                     Query Match 90.3%; Score 1195; DB 2; Length 613; Best Local Similarity 100.0%; Pred. No. 3.8e-123; Matches 227; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with TITLE OF INVENTION: Increased Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pastan, Ira H. APPLICANT: FitzGerald, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,709
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                          TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 PRREKRWSEWASGKVLCLLDPLDGVYNYLAQORCNLDDTWEGKIYRV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/463,480 FILING DATE: 05-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Califo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Embarca
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
STRANDEDNESS:
                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                  AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGOGVLHYSMVLEGGNDALKLAI 85
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                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                               613 amino acids
                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                            : protein
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                                                                                                                                       Gaps
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US-08-225-224-1
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                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: Protein
; LOCATION: 1..614
; OTHER INFORMATION: /label- native-PE
US-08-225-224-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-9643
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08225224 Patent No. 5635599
                                                                                                                                                                                                                                                     Query Match 90.3%; Score 1195; DB 1; Best Local Similarity 100.0%; Pred. No. 3.8e-123; Matches 227; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,224
FILING DATE: 8-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PASTAN, Ira
APPLICANT: KREITMAN, Robert J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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146 NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                         26 AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGGGVLHYSMVLEGGNDALKLAI 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                     2 AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGKIYRV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ
                                                                                    DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
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                                                                                                                                                                                                                                                                                               Length 614;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                        Matches
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Circularly Permuted Ligands and TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,762
REFERENCE/OOCKET NUMBER: 015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-APR-1995
PRIOR APPLICATION UNMEER: US 08/225,224
FILING DATE: 08-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: V
                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
     146
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SOFTWARE: PatentI
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CITY: San Francisco
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                                                                                                                                                                                                                                                                      LOCATION: 1..614
OTHER INFORMATION:
OTHER INFORMATION:
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                                     62
                                                                     98
                                                                                                                     26 AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGGGVLHYSMVLEGGNDALKLAI 85
                                                                                                                                                                      Local Similarity 100.
mes 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein LOCATION: 1..614
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 NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ 205
                                                                                                   AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAI 61
                                   DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 121
                                                     DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
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                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                             614 amino acids
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Puri, Raj K.
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                                                                                                                                                                                                                                                                                                                                                                             linear
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08-JAN-1997
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                                                                                                                                                                                                                                                                                            /note= "native Pseudomonas exotoxin
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                                                                                                                                                                                        Score 1195; DB 3; pred. No 3.8e-123;
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PCT-US95-04468-1
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; OTHER INFORMATION:
PCT-US95-04468-1
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                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                   Best
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 614 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/225
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600
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                                                                                    146
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 07-APR-1995
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: un
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                                                                                                            62
                                                                                                                                                              Local Similarity
les 227; Conserv
                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein LOCATION: 1..614
                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
                                                                                                                                       98
                                                      DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 121
                                                                                                                          DNALSTTSDGLTIRLEGGVEDNKPVRYSYTROARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                        unknown
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                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                     90.3%; Score 1195; DB 5;
100.0%; Pred. No. 3.8e-123
/ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                     /label= native-PE
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US-09-046-992-2; Sequence 2, Application US/09046992

Burn, Timothy C.

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US-08-665-259-25
; Sequence 25, Application US/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
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; FRAGMENT TYPE:
US-09-046-992-2
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NAME: POISSANT, Brian M
REGISTRATION NUMBER: 28.462
REFERENCE/DOCKET NUMBER: 9457
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: Yarkoni, Shai
APPLICANT: Yarkoni, Shai
APPLICANT: Ben-Yehudah, Ahmi
TITLE OF INVENTION: METHODS OF CANCER DIAGNOSIS
TITLE OF INVENTION: USING A CHIMERIC TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
APPLICANT:
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CITY: New York
STATE: NY
                                                                                                                             199 VVMAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGKIYRV 252
                                                                                                                                                                                              136 KVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COMPALIALE
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                           139 KVFIHELNAGNOLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMOPTLAISHAGVS 198
                                                                                                                                                                                                                                                                           79 DALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 24-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds, LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                             16
                                                                                                                                                                                                                                                                                                                                              19 GGSSASAAEEAFDLWNECAKACYLDLKDGVRSSRMSVDPAIADTNGOGVLHYSMYLEGGN 78
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                              DALELAIDNALSITSDGLTIRLEGGVEPNKPLRYSYTRQARGRWSLNWLVPIGHEKPSNI 135
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Landes, Gregory M.
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95.3%;
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                                                                                                                                                                                                                                                                                                                                                                                           Score 1181; DB 4;
Pred. No. 1.4e-121;
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RESULT 10
US-08-762-500-25
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                                                                                                                                                                                                                                              Sequence 25, Application US/08762500 Patent No. 6030806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING,
NUMBER OF SEQUENCES: 73
                                APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy D.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING,
NUMBER OF SEQUENCES: 83
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REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IG
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: 17-JUN-199
CLASSIFICATION: 435
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LENGTH: 1684 amino acids
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                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                              203 QTQPRREKRWSEWASGKVLC-LLDPLDGVYNYLAQQR 238
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STATE: Macco
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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ADDRESSEE:
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GENZYME CORPORATION
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22.9%;
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4.

One Mountain Road

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-762-500-25
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Best Local Similarity
                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                          Sequence 75,
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
ODERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,259
FILING DATE: 17-JUN-1996
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                                                                                                 APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Kiinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16
TITLE OF INVENTION: COMPOSITIONS, METHODS OF M.
NUMBER OF SEQUENCES: 83
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                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 LLAKLARDATFFVRAHESNEMQPTLAISHAGVSVV------
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CITY: Framingham
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                 STREET: OLC CTTY: Framingham
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                                                                 ADDRESSEE: GENZYME CORPORATION
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                                                 One Mountain Road
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, 872-5415
, NO: 25:
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States of America
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imothy C.
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                                                                                                                          HROMOSOME 16 GENES,
METHODS OF MAKING
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; MOLECULE TYPE: protein US-08-762-500-75
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Best Local Similarity 22.9%;
Matches 36; Conservative 2
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                                                                                                                                                                                                                                                                                                                                    Patent No.
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                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: DUGAN, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10469
FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
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APPLICANT:
APPLICANT:
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CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US_08/665,259
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                   APPLICANT:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 QTQPRREKRWSEWASGKVLC-LLDPLDGVYNYLAQQR 238
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COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                COUNTRY:
                                                                                                  STATE:
                                                                                                                   CITY:
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                                                                  ZIP: 02140
                                                                                                                   Cambridge
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                                                                                     USA:
                                                                                                                                                                                                                   Whitters, Matthew Wood, Clive
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                                                                                                                                                                                                                                                                      Fitz, Lori
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SYSTEM: PC-DOS/MS-DOS
   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                   Floppy disk
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58;

Gaps

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-609-572-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9
COMBREGORIANTE
                                  ATTORNEY/AGENT INFORMATION:
                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
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REGISTRATION NUMBER: 32,724
                                                                                                          CLASSIFICATION:
                                                                                                                               FILING DATE:
                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                COUNTRY:
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Neben, Tam
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20.7%; Pred. No. 0.23;
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Best Local Similarity
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                               TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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LENGTH: 380 amino acid
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Floppy
                                                                                       REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
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NAME: Brown, Scott A.
                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ZIP: 02140
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STREET: 87 CambridgePark Drive
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Fitz, Lori
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(617) 876-5851
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20.7%; Pred. No. 0.
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Best Local Similarity
Matches 34; Conserv
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Query Match
Best Local Similarity 20.7
Matches 34; Conservative
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APPLICANT: Collin:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TYPE: amino acid
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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 6152
REFERENCE/FOCKET NUMBER: 6152
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10F0RMATION:
TELECOMMUNICATION 10F0RMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
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CORRESPONDENCE:
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APPLICATION NUMBER: (
FILING DATE:
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 6.7%; Score 88; DB 4; Length 380; 20.7%; Pred. No. 0.23; tive 26; Mismatches 46; Indels
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GenCore version (c) 1993 - 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapext 0.5
                                      chosen parameters:
           RA30367
RA30367
RA59188
RS71363
RS9188
RS71363
RS3599
RS209900
RS209901
RS20901
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Compugen Ltd
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                                                                                                                                     pyruvate carboxyla
hypothetical prote
cleavage and polya
urease (EC 3.5.1.5
transient axonal g
exported serine pr
                                                                                                                                                                                                                                                                  hypothetical prote
hypothetical prote
titin - mouse (fra
probable replicati
                                                                                                                                                                                                                          hypothetical prote
titin - rabbit (fr
titin, cardiac mus
                                                                                                                                                                                                                                                                                                                                         exotoxin A precurs
           pyruvate carboxyla
probable RTX famil
                                    pyruvate carboxyla
nitrilotriacetate
                                                                                                 erythroid
                                                                                                              nucleocapsid prote multiple PDZ domai
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probable ATP-bindi
                                                                                                                                                                                                                 hypothetical prote
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                                                             nucleocapsid
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                                                                                     hypothetical prote
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                                               psid protein
carboxyla
                                                                                                  ankyrin
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exotoxin A precursor PA1148 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa (C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: C83503 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,

RESULT C83503

δÃ DЬ Qy В

LDDTWEGKIYRV

252 252

181 181

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241

LDDTWEGKIYRV

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121

121

Qy

В

MHLIPHWIPLVASLGLLAGGSSASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA

MHLIPHWIPLVASLGLLAGGSSASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA

60 60

DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG 120

DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG

SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA 180

HESNEMOPTLAISHAGVSVVMAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN

HESNEMOPTLAISHAGVSVVMAQTOPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN

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61 61 Н

| Ouery Match Best Local Similarity Matches 252; Conser | RESULT 1 A30347 A30347 A30347 A30347 C; Species: Pseudomonas aeruginosa C; Late: 08-Jun-1990 #sequence_revision 08-Jun-199 C; Accession: A30347 R; Gray, G.L.; Smith, D.H.; Baldridge, J.S.; Harki Proc. Natl. Acad. Sci. U.S.A. 81, 2645-2649, 1984 A; Title: Cloning, nucleotide sequence, and expres A; Reference number: A30347; MUID:84194063 A; Accession: A30347 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-638 GGRA> A; Cross-references: GB:K01397; GB:M23348; NID:g15 C; Superfamily: Pseudomonas aeruginosa exotoxin A C; Keywords: exotoxin | | 30 82.5 31 82 32 82 33 81.5 35 81.5 36 81 37 81.5 38 81 40 81 40 80.5 42 80.5 80 |
|--|--|------------|--|
| 100 dilarity 100 Conservative | precursor - Ps. Pseudomonas ae Jun-1990 #sequ. : A30347 Acad. Sci. U. Acad. Sci. U. oning, nucleot oning, nucleot inumber: A3034 : A30347 reliminary type: DNA 1-638 <gra> erences: GB:KO 1y: Pseudomona exotoxin</gra> | | 6.00 |
| 100.0%; 100.0%; tive | Pseudomonas aeruginosa aequence_revi .H.; Baldrid U.S.A. 81, potide seque 0347; MUID:8 | | 344 325 338 1807 274 281 401 401 788 997 1295 1034 11034 11034 11700 898 |
| | ona: osa osa frev dri: 81, 81, equ iD: | | |
| Score 1323; DB 2; Length Pred. No. 9.7e-109; O; Mismatches 0; Indels | 0 #te: ns, R sion : | ALIGNMENTS | F83620 B69786 T36025 T26319 E75303 PNSAP PNSAP S15239 S15239 S15239 T124587 T24587 T32814 T32814 T32816 T32816 T32817 T32 |
| | change 24-N; Vasil, M.; Vasil M. Escherichia | | probable bind thiamin-monoly conserved by integrin betty citrate lyass beta-lactama: hypothetical anthranilate speract receip hypothetical sodium channocodium channocodium channoprobable invhypothetical hypothetical sodium channocodium channocodium channoprobable invhypothetical hypothetical hypothetical hypothetical hypothetical |
| 638; 0; | 24-1 1, M 1, M 1; Chia | | able arvections in the tract in the tract in the tract in the track in |
| Gaps | ext_change 24-Nov-1999 R.N.; Vasil, M.L.; Chen, E.Y.; in Escherichia coli of the ex ; PIDN:AAB59097.1; PID:g151216 | | probable binding p thiamin-monophosph conserved hypothet integrin beta 4 ch citrate lyase, bet beta -Lactamase (EC hypothetical prote anthranilate synth speract receptor p hypothetical prote hypothetical prote sodium channel alp sodium channel alp probable invasin 2 hypothetical prote |
| 0; | the exot | | , |

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; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337
A;Accession: C83503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: \bar{1}-638 <STO> A;Cross-references: GB:AE004544; GB:AE004091; NID:g9947060; PIDN:AAG04537.1; GSPDB:GN00 A;Experimental source: strain PA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: toxA; PA1148
C; Superfamily: Pseudo
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                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A59188
R;Connors, T.D.; van Raay, T.J.; Petry, L.R.; Klinger, K.W.; Landes, G.M.; Burn, Genomics 39, 231-234, 1997
A;Title: The cloning of a human ABC gene (ABC3) mapping to chromosome 16p13.3.
A;Reference number: A59188; MUID:97179225
A;Accession: A59188
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                                                                                                                                                                                                                            A;Cross-references: GDB:3770735; OMIM:601615
A;Map position: 16p13.3-16p13.3
C;Superfamily: ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:U78735; NID:g1699037; PIDN:AAC50967.1; PID:g1699038 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-1704 <CON>
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Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Species: Homo sapiens (man);Date: 18-Feb-2000 #text_change 04-Mar-2000;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 98.8%;
Best Local Similarity 98.8%;
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Best Local Similarity
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                                                                                                      114 YTRQARGSWSLNWLVPIGHEKPSNIKVFIH------ELNAGNQLSHMSPIYTIEMGDE 165
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                                                                      749
                                 166 LLAKLARDATFFVRAHESNEMQPTLAISHAGVSVV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDDTWEGKIYRV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HESNEMOPTLAISHAGVSVVMAQTOPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG
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                                                                   FLKQKYGAGYHMTLVKEPHCNPEDISQLVHHHVPNATLESSAGAELSFILPRESTHRFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA
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                                                                                                                                           Conservative
                                                                                                                                                        7.1%;
22.9%;
   EKKQKELGIASFGASITTMEEVFLRVGKLVDSSMDIQAIQLP
                                                                                                                                             22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1307; DB 2;
Pred. No. 2.5e-107;
0; Mismatches 3;
                                                                                                                                                              Score 93.5;
Pred. No. 12;
                                                                                                                                                                               DB 2;
                                                                                                                                               54;
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                                                                                                                                                                               Length 1704;
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A;Cross-references: GDB:3770735; OMIM:601615
A;Map position: 16p13.3-16p13.3
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding C;Keywords: ATP binding; nucleotide binding; P-loop; phosphoprotein; F;255-283/Domain: transmembrane #status predicted <TM1>F;345-364/Domain: transmembrane #status predicted <TM3>F;345-364/Domain: transmembrane #status predicted <TM3>F;345-364/Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1100-1120/Domain: transmembrane #status predicted <TM7>
F;1145-1169/Domain: transmembrane #status predicted <TM8>
F;1181-1207/Domain: transmembrane #status predicted <TM9>
F;1181-1207/Domain: transmembrane #status predicted <TM1>
F;1215-1236/Domain: transmembrane #status predicted <TM11>
F;1245-1246/Domain: transmembrane #status predicted <TM11>
F;1299-1324/Domain: transmembrane #status predicted <TM12>
F;1399-1590/Domain: drp-binding cassette homology <ABC2>
F;1399-1590/Domain: Amp-binding cassette homology <ABC2>
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FEBS Lett. 391, 61-65, 1996
A;Title: Primary structure of a novel ABC
A;Reference number: S71363; MUID:96326608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1346-1423/Region: nucleotide binding motif A (P-loop)
F;1535-1540/Region: nucleotide-binding motif B
F;674,866,1524/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent F;1344/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;549-739/Domain:
F;566-573/Region:
F;685-690/Region:
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F; 401-422/Domain:
F; 452-475/Domain:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                           114 YTROARGSWSLNWLVPIGHEKPSNIKVFIH-----ELNAGNQLSHMSPIYTIEMGDE 165
                                                                               203 QTQPRREKRWSEWASGKVLC-LLDPLDGVYNYLAQQR 238
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les 36; Conserv
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ALQYQHERRASDWAVDSNLCGAMDPSDGIGALIEEER
                                                                                                                                                                                                                                                                                                                                                   FLKQKYGAGYHMTLVKEPHCNPEDISQLVHHHVPNATLESSAGAELSFILPRESTHRFEG 808
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transmembrane #status predicted <TM5>
transmembrane #status predicted <TM5>
transmembrane #status predicted <TM5>
ATP-binding cassette homology <ABCl>
nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane #status predicted <TM1>
transmembrane #status predicted <TM2>
transmembrane #status predicted <TM3>
transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%;
22.9%;
                                                                                                                                                                                -EKKQKELGIASFGASITTMEEVFLRVGKLVDSSMDIQAIQLP 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                      -MA 202
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C:Species: phage SPP1
C:Date: 25-Dec-1994 **sequence_revision 26-May-1995 **text_change 17-Nov-2000
C:Date: 25-Dec-1994 **sequence_revision 26-May-1995 **text_change 17-Nov-2000
C:Accession: $43799; T42331; S41173
R:Pedre, X.; Weise, F.; Chai, S.; Lueder, G.; Alonso, J.C.
J. Mol. Biol. 236, 1324-1340, 1994
A:Title: Analysis of cis and trans acting elements required for the initiat. A:Reference number: $43798; MUID:94172631
A:Accession: $43799
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X67865; NID:g472886; PIDN:CAA48050.1; PID:g439630 A;NOte: the nucleotide sequence was submitted to the EMBL Data Library, July R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A. Gene 204, 201-212, 1997
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A;Residues: 1-4180 <5TO>
A;Cross-references: GB:AE004504; GB:AE004091; NID:g9946568; PIDN:AAG04079.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adman, S.; Yuan, Y.; Brody, L.L.; .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                        A;Title: The complete nucleotide sequence and functional A;Reference number: 222137; MUID:98094274 A;Accession: T42331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337
                                       Ş
                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-311 <PED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 34.1 - phage SPP1
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R; Stover, C.K.; Pham, X.Q.;
  밁
                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X97918; PIDN:CAA66538.1
                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain PAO1
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                                                                                                                                                                          Query Match
Best Local S
Matches 35
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Best Local S
Matches 50
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                                                                                                                                                                                                                                                                                                          Molecule type: DNA Residues: 1-136,'Y',138-311 <ALO>
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  151
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                                                                                                                              52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA0690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SASLYSGALGGIDPRYDTLLRDPA-EVRSRDA--FSPTLASSTGGLTLVAGDTGMRLETR 3421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSPIYTIEMG---DELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQPRREKR 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLNVRIGGEVNPSREARATQTYSSSG---FDGLYSGG-----TIHDLQGALINLRG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL-NAGNQLSH 153
                                       RYSYTROARGSWSLNWLVPIGHEKPSNIKV-----FIHELNAGNOLSHMSPIYTIEMGD 164
                                                                                                                              RMSVDPAIAD-TNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGGGNLSMRTGGDAGNIAPRGDGSIPSSGNLNPRSQGLVLAVAGTGRLTSDGALQLGGGG 3316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
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  -YMIQVQH---
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                                                                                                                                                                          21;
                                                                                                                                                                       Score 90.5; DB Pred. No. 2.1; 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93.5;
Pred. No. 40;
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  -NIKVVEADFAYVVALIGGNKYKH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                     В
                                                                                     -IKTASESLKEEWEGEDIPNQ-- 150
                                                                                                                                                                            44;
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                                                                                                                                                                                                                   Length 311;
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-YYIERDD
                                                                                                                                                                            51;
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Larbig, K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1992
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probable replication licensing factor MCM6 - Caenorhabditis elegans N;Alternate names: hypothetical protein ZK632.1 C;Species: Caenorhabditis elegans C;Date: 06-Jan-1995 #sequence_revision 19-Jul-1996 #text_change 24-S;C;Accession: S40933 R;Berks, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X64700; NID:g54807; PIDN:CAA45941.1; PID:g54808 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Fet C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin C;Keywords: muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C;Accession: S20900
R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A;Title: Towards a molecular understanding of titin.
A;Reference number: S20897; MUID:92258380
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C;Superfamily: cyclopropane-fatty-acyl-phospholipid C;Keywords: cell cycle control; DNA replication; me' F;1-365/Domain: MCM homology (fragment) <MCM>
                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z22181; NID:g297998; PID:g297999 C;Comment: The complex of six MCM proteins is one of seve
                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, February 1993 A; Reference number: $\rm S40933
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A; Residues: 1-531 <LAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: $20900
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                                                                                                                                     A; Map position: 3
A; Introns: 463/2
                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-521 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown; translation not shown
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                                                                     A; Description: part of the replication licensing system that permits DNA replication
                                                                                                C; Function:
                                                                                                                   C; Complex: The predominant form is a heterohexamer
                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                     A; Accession: S40933
                                                                                                                                                                                                                                                                                                                                                      A; Reference number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 DPAIADTNGQGVLHYSMVLEGGN--DALK--LAIDNALSITSDGLTIRLEGGVEPNKPVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSKIIQYIVEMQAKNTDKWSECARVK-----SLDAVITNLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSVV----MAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAAIIDVTSS---FTSLVLDNVNRYDSGKYTLTLENSSGTKSAFVTVRVLD--TPSPPVN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELLAKLARDATFFVRAHESNEMOPTLAISHA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGCSYYFRVTAENEYGIGLAARTADPIKVAEVPQPPGKITVDDVTRNSVSLSWTKPEHDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDATFFVRAHESNEM-----HAG 196
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                        methyltransferase;
                                                                                                                   of MCM2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 531
                                                                                                                                                                                                                                          several
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                                                                                                                   MCM3,
                                                                                                                                                                                                                                       proteins that must
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                                                                                                                   MCM4, MCM5,
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                                                                                                                      MCM6,
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C;Specie
C;Date:
C;Access
R;Lye,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 31-Jan-2000
C;Accession: T39131; T41433; S62525
R;Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL032824; PIDN:CAB37424.1; GSPDB:GN00068; SPDB:SPCC584.11c A;Experimental source: strain 972h-; cosmid c584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated A;Molecule type: DNA A;Residues; 1-380 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z66569; NID:g1052533; PIDN:CAA91519.1; PID:g1052540; R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, October 1998 A;Reference number: Z21993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T39131
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z21830
A; Accession: T39131
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           RESULT
S20901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: T41433
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Best Local S
Matches 55
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titin
                                                                                                                                                                                                                                                                                                                                                                                   Gene: SPCC584.11c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :Gene: SPAC8A4.09c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics: <SEE1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 DQVAIHEAMEQQ-TISITKAGVKATLN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
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                                                                                    368
                                                                                                                                                                                                                                                 71 SMYLEGGNDALKLAIDNALSITSDGLTIRLEGGVEP----NKPVRYSYTRQARGSWS--- 123
                                                                                                                                                                                                                                                                                                                Local Similarity
                                 10
rabbit (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAGGSSASAAEEA--FDLWNECA---KACVLDLKDGVRSSRMSVDPAIADTNGQ-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVGGDASGAVEETDYLDLWSKMSTEDRATLKKMSDDKKIEKNIVDSLFPNIYGNHEVKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFVRAHESNEMOPTLAISHAGVSVVMAQTQPRREKRWSEWASGKVLCLLDPLDGVYN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDAT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEG------GVEPNKPVRYSYT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SGKASSAAGLTAAVVKDEES----FEFVIEAGALMLADNGVCCIDEFDKM------DLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VL---LMLLGG--VAKKSRDEGTSLRGD-INVCLVGDPSTAKSQVLKAVEEFSP-RAIYT 131
                                                                                                                                                   DIHLSVDAPLGRRLQRIDVLAEIPSWLKGFVHGVSGTKPFIYQYFSPVKFTLKMGDEVIE
                                                                                                                                                                                        ---LNWLVPIGH------EKPSNIKVFIHELNAGNQL--SHMSPI-YTIEMGDELL- 167
                                                                                                                                                                                                                         STIVNIGGIAMK----DKIISATVDNTIEHVETTLDPDTEWHEPTRISYEWDGKDAETYTE
                                                                                    DEATLFNETTF 378
                                                                                                                      --AKLARDATF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe
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55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <LYE1>
                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                 26;
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                                                                                                                                                                                                                                                                                                                Score 89; DB 2;
Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                     Length 380
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C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C:Accession: S20901; 146520
R:Clabeit, S:, Gautel, M., Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A:Title: Towards a molecular understanding of titin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-6805 <LAB>
A;Residues: 1-6805 <LAB>
A;Cross-references: EMBL:X64696
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Labelt, S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.; Francke, U
R;Labelt, S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.; Francke, U
Nature 345, 273-276, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA A;Residues: 4235-5250 <LA2> A;Residues: 4235-5250 <LA2> A;Cross-references: EMBL.X17329; NID:g1756; PIDN:CAA35207.1; PID:g930251 C;Superfamily: titin; fibronectin type III repeat homology; immunoglobul C;Keywords: muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: A regular pattern of two types of 100-residue motif in A; Reference number: T46520; MUID:90238553
A; Accession: T46520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Sep-2000
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Sep-2000
C;Accession: I38344; I38345; S20898; S20897; S20899; S63665; S37393
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                                                                                                                       A;Cross-references: EMBL:X90568; NID:g1017424; PID:g1017425
R;Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.
Biochemistry 34, 553-561, 1995
Biochemistry 34, 553-561, 1995
A;Title: Dissecting titin into its structural motifs: ident:
A;Reference number: 138345; MUID:95119041
                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity. A; Reference number: A57430; MUID:96026330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate names: connectin
            A; Molecule type: mRNA
A; Residues: 1977-2014 <MUS>
                                                                                           A; Reference number:
A; Accession: 138345
                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-26926 <LAB1>
                                                                                                                                                                                                                                                                                                                                                          A; Accession: I38344
                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 270, 293-296, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Labeit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       titin, cardiac muscle [validated] -
                                                                      A;Status: nucleic
                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 YSYTROARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity les 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKYTEITKDSVSITWEPPL-LDGGSKIKNYIVEKRDSTRKSYAAVVTNCHKSSWKIDQLQ 4960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGCSYYFRVTAENEYGIGLPARTADPIKVAEVPQPPGKITVDDVTRNSVSLSWTKPEHDG
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                                                                         acid sequence not shown
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22.1%;
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Pred. No. 1.9e+02;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                          translation not shown; translated from
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PID:g602580
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A; Cross-references: EMBL: X83270;

NID:g602579; PIDN:CAA58243.1;

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A:Residues: 26729-26825 <KOL>
A;Cross-references: EMBL:X92412; NID:g1236761
R;Gautel, M.; Leonard, K.; Labeit, S.
EMBO J. 12, 3827-3834, 1993
A;Title: PhosphoryLation of KSP motifs in the A:Reference number: S37393; MUID:94008990
A;Accession: S37393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structural protein
F;24752-25008/Domain: protein kinase homology <KIN>
F;84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,4068,
F;84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,4068,
98,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,13540,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: structural protein forming filaments in striated muscle C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; pro C;Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Brookhaven Protein Data Bank, August 1996 A;Reference number: A66201; PDB:1NCT A;Contents: annotation; conformation by (1)H-NMR, residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 26831-26926 <GAUS
R; Improta, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, February 1996
A; Reference number: A66736; PDB:1TIT
A; Contents: annotation; conformation by (1) H-NMR, residues 52
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A:Accession: S63665
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A; Residues: 'P',22278-22431,'R',22433-22448,'G',22450-22453,'Q',22455-22480,'TR',
A; Cross-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195
R; Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S.
J. Mol. Biol. 256, 556-563, 1996
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A;ResIdues: 16330-16382,'S',16384-16756,'F',16758-16860 <LAB3>
A;Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1;
A;Accession: S20899
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A;Map position: 2q31-2q32
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A; Residues: 26729-26
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EMBO J. 11, 1711-1716, 1992
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Best Local Similarity
Matches 46; Conserv
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                                                                                                                 16488
  16543
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                                                     YSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLA 171
                                                                                                              DAATIDVTSS---FTSLVLDNVNRYDSGKYTLTLENSSGTKSAFVTVRVLD--TPSPPVN 16542
                                                                                                                                                                    DPAIADTNGQGVLHYSMVLEGGN--DALK--LAIDNALSITSDGLTIRLEGGVEPNKPVR 111
LKVTEITKDSVSITWEPPL-LDGGSKIKNYIVEKREATRKSYAAVVTNCHKNSWKIDQLQ 16601
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                        6.7%; Score 89; 1
22.1%; Pred. No. 1
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                                                                                                                                                                                                                                                                                   RESULT 13
T43735
                       Insect Biochem. Mol. Biol. 27, 133-147, 1997 A;Title: Biochemical, molecular, and phylogenetic A;Reference number: Z22655; MUID:97218699 A;Accession: T43735
                                                                                                                                                                                            pyruvate carboxylase (EC 6.4.1.1) [validated] - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Au
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R;Tu, Z.; Hagedorn, H.H.
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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hypothetical protein F20D1.6 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tv C:Accession: T21147 R:Burton, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, August 1996 A;Reference number: Z19382 A;Accession: T21147 A;Status: preliminary; translated from GB/EMBL/DBJA;Status: preliminary;
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A;Introns: 45/3; 75/3; 126/3; 166/2; 196/3; 243/3; 271/2; 321/1;
C;Superfamily: Caenorhabditis elegans hypothetical protein F20D1
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A; Residues: 1-915 <WIL>
A; Cross-references: EMBL: Z78542; PIDN: CAB01748.1; GSPDB: GN00028; CESP: F20D1
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                                                                                                                                                                                                               KPSNIKVFIHELN-----AGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEM 186
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LQCS
                                         QRCN 240
                                                                                                                                                                      AESDNESLAHELNMLNAASMSENQLSDDELVNNVKLDTLFNYKNPKSANTFLAPYKCAKK 461
                                                                                                                                                                                                                                                               QKLTINSASEVKIGKHAETEDSGT
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                                                                                      STVTWRLAIALANARVFMSD-QPRAEPQLWVEF----LLKLREKYEKMETVEKVYNGIDH 516
                                                                                                                             QPT----LAISHAGVSVVMAQTQPRREKR-WSEWASGKVLCL-----LDPLDGVYNYLAQ
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22.7%;
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Pred:
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analysis

of

pyruvate

carboxylase

#text_change 18-Aug-2000

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A; Molecule type: mRNA
A; Residues: 1-1195 <TUZ>
A; Cross-references: EMBL:L36530; PIDN:AAB64306.1
A; Cross-references: EMBL:L36530; PIDN:AAB64306.1
C; Function: EC 6.4.1.1 [validated; MUID:97218699]
A; Description: EC 6.4.1.1 [validated; MUID:97218699]
C; Superfamily: pyruvate carboxylase; biotin carboxylase homolog
C; Keywords: ligase
C; Keywords: ligase
F; 1161/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference number: A86141; MUID:21016719

A,Accession: F86182
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C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
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A; Residues: 1-1064 <STO>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    752 THILCIKDMAGLLKPQAAKLLIAAIREKHPDVPIHTHTHDTSGAGVASMLACAEAGADVV 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 6.7%; Score 88; DB Local Similarity 21.6%; Pred. No. 22; nes 50; Conservative 34; Mismatches
                                                                                                                                                                                                  601 HGLPMVATKNGGPVDIHRALHNGLLVDPHDQEAIANALLKLVSEKNLWHECRINGWKNIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
                                                                                               661 LFSWPEHCRTYLTRIAAC-----RMRHPQWQTD---ADEVAAQDDEFSL-----NDSLK 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MHLIPHWIPLVASLGLLAGGSSASAAEEAF------
                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTTMKSGNADVYLNEIPGGOYTNLQFQAYSLGLGDFFEDVKKAYREANLLL 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GHEKPSNIKVFTHELNAGNQLSHMSPIYTIEMGD--ELLAKLARDATFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVAVDSMSGMTSQPSMGAVVASLQGTPLDTGLNLRDISEYSAYWEQTRTLYA-----PFE 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLAIDNALSITSD---GLTIR-----LEGGVEPNKPVRYS-YTRQARGSWSLNWLVPI- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CVLDLKD------GVRSSRMSVDPAT--ADTNGQGVLHYSMVLEGGNDAL 81
                                             LAIDNALSITSDGLTIRLEGGVEPNK--PVRYSYTRQARGSWSLNWLVPIGHEKPSNIKV 140
                                                                                                                                                                                                                                                     HWIPLVASL------
     DVQDMSLRLSMDGDKPSLNGSLEPNSADPVKQIMSRMR
                                                                                                                                                                                                                                                                                                       . Similarity 21.1 60; Conservative
                                                                                                                                                  -AKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALK 82
                                                                                                                                                                                                                                                                                                                               6.6%;
                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                       -GLLAGGSSASAAEEAF-----DLWNEC------
                                                                                                                                                                                                                                                                                                                               Score 87; DB 2; Length 1064; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biotin carboxylase homology; lipoyl/biotin-binding
                                                                                                                                                                                                                                                                                                             Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DLWNECAKA- 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1195
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          -TPEIKSKP----
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C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57335; S57333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S57335; S57333
R;Jenny, A; Keller, W.
Nucleic Acids Res. 23, 2629-2635, 1995
Nucleic Acids Res. 23, 2629-2635, 1995
A;Title: Cloning of cDNAs encoding the 160
A;Reference number: S57333; MUID:95380277
A;Accession: S57335
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A;Residues: 1-1444 <JEN>
A;Cross-references: EMBL:X83097; NID:g953171; PIDN:CAA58152.1; PID:g929007
A;Accession: S57333
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                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 188-197;204-216;403-423;426-437;511-519;573-580;780-789;1107-1116;1163-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            804 KAVRSDPQMAKN-----SGFAISTSMPLDELTRFLKSAKIQVSE 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 FIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVV
                                      206
                                                                            463
                                                                                                                158
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                                                                                                                                                                                                                              358
                                                                                                                                                                                                                                                                                                     298 PYGVALNSLTTGTTAFPLRTQEGVRITLDCAQAAFISYDKMVISLKGGEIYVLTLITDGM 357
                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                         9 PLVASLGLLAGGSSA--SAAEEAFDLWNECAKAC------VLDLK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MA-QTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ELQGKKQSDNLGSKYPVLRRERLVVLAVDCYDNEGAPDEKAMVPMIQ----
                                                                                                                                                                                                                                                              RSSR-MSVDPAIADTNGQGVLHYSMV-LEGGNDALKLAIDNALSI-----TSDGLTIR
PQ 524
                                                                          YSFEVCDSILNIGPCANAAMGEPAFLSEEFQNSPEPDLEIVVCSGYGKNGALSVLQKSIR 522
                                                                                                              YTIEMGDELL----AKLARDATFFVRAHESNEMQPTLAI-----SHAGVSVVMAQTQ 205
                                                                                                                                                    EAADKEEPPSKKKRVDATT----GWSGSKSVP--QDEVDEIEVYGSEAQSGTQLA----T
                                                                                                                                                                                    LEGGVE--PNKPVRYSYTROARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNOLSHMSPI 157
                                                                                                                                                                                                                          RSVRAFHFDKAAA-----SVLTTSMVTMEPGYLFLGSRLGNSLLLKYTEKLQEPPASTAR 412
                                      PR 207
                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   6.6%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 87; DB 2; Length 1444; Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                       92;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                       DGV
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SwissProt_39:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93435 seqs, 34255486 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-412-558-3
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        GenCore version Copyright (c) 1993 - 2000
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HATZ_YEAST
GAS7. HUMAN
GAS7. MOUSE
NIFD_METBA
TRPC_PHACH
CYGR_ARBPU
THIM_BACSU
DCAM_HELAN
DCAM_HELAN
URSI_USTMA
PIMT_MOUSE
K6PL_HUMAN
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CPSA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                TOXA_PSEAE
ABC3_HUMAN
MW6_CAEEL
YC9B_SCHPO
1132_HUMAN
CPSA_BOVIN
URE2_HELPY
AXO1_HUMAN
VNUC_MABVM
THIL_BACSU
1TB4_RAT
BLAC_STAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homo sapien
marburg vir
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| Z X | R R X | RPR | R Z | 목 | R X | RP | | | | | | R R | RE S | R R | RA 3 | RA | R R A | RAS | 2 2 | RP A | 뫋 | R R | RA | RX | R R | 2 | 88 | 20 | S D | DE | D D | DT AC | TOXA | RES | | | | | | | | |
|--------------|---|---------|----------------------------|---------------------|------------------------------|---------|-----------|---------------------------------|----------------|----------|----------|----------|----------|---------------------|--------------------|--------------------|--|---|----------|----------|----------------|--|---------------------------|----------------|--------------|----------|----------------------------|-------------------------|------------|--------------------|-------------------------|---------------------|------------------|-----|------------|----------------------------|------------|------------|----------------------------|-------------|-------------|-------------|
| evot | Bourden | DOMAINS | 7 . E | "Mut | Chau | DOMAINS | J. | ació | is t | Cari | MEDI | [E] | Natu | "Con | Reiz | Broc | Gark | Stov | STRA | SEQU | Proc | the "Clo | Chen | MEDI | SEQU | NCBI | Bact | Pseu | ETA ETA | EXOI | 01-0 | 01-C | A_PSEAE TOXA_ | | | 44 | 42 | 40 | ယ ယ ဖ စ | 37 | 3 3 6 | 3 4 |
| orin A f | EDLINE=91006124; PubMourdenet S., Vacheron | | iol. Che | "Mutagenesis of | MEDLINE=903/ Chaudhary V. | INS. | liol. Che | acid 148 of diphtheria toxin."; | hotolabe | Oll S.F. | INE=8725 | duto da. | re 406:9 | plete ge | er J., s | ly L.L., | er R.L., | er C.K., | IN-PAO1; | ENCE FRO | . Natl. | exotoxin | Chen E.Y., Heyneker H.L.; | INE=8419 | SEQUENCE FRO | _TaxID=2 | eria; Pr domonas. | Pseudomonas aeruginosa. | 2.4.2) | OXIN A P | 01-OCT-2000 (Rel. 40, 1 | 39; Q914 CT-1989 | PSEAE | _ | | 75.5 | 76 | 76 76 | 76 76 | 76 | 76.5 | 76.5 |
| rom Ps | , Vach | | m. 265 | of Ps | -903/5493; cy V.K., Ji: | | m. 262 | diphth | led by | , coll | 0491; 1 | | 59-964 | nome se | aier M | Coulter | Goltry | Pham : | 7227. | M N.A. | Acad. | cleotic | eyneke | 4063; 1 | X 2. A. | 287; | oteobac | aerugin | »÷ | RECURSO | (Rel. | I7; (Rel. 1 | STAN | | | 5.7 | - | | | | | |
| Psendomona | PubMed=217012 eron MJ., G | | :16306- | eudomon | nno Y., Galo M. | | :8707-8 | eria to | NAD an | ier R.J | PubMed≖ | | (2000). | equence | .н., на | S.N. | nan F.S | KQ.T. | | | Sci. U. | de sequ | . H.L.; | PubMed=6201861 | AND S | | cteria; | • | | OR (NAD | 10, Last se | 12, Cre | STANDARD; | | | 474 | | | | | | |
| e E | 217 -J. | | 163 | as - | Ga | | 711 | Xin | o d | : . | 288 | | | 0f | D 20 | Б | ole | , E | 9 | | S.A | ence | 101 | 620 | EQUI | | gai | | | -DEI | t Se | ated | | | | P P F | | | | | | |
| ear stu | ; PubMed=2170123; cheron MJ., Guinand M. | | em. 265:16306-16310(1990). | exotoxi | 10 M.G. | | (1987). | = (| shows funct | | 5323; | | | Pseudor | CK 8.E. | lger K.I | , Hurnaç ntino E | rwin A. | 040. | | . 81:26 | e, and en | | - | ENCE OF | | gamma subdivi | | | PENDENT | equence | <u>.</u> | PRT; | | ALIG | TYPH_METJA | YAA_BOF | RPO ROT | MCS_ARA | TF2D_CAEEL | PRLR_HUMAN | SELB ECC |
| or broceotyc | , Michel G., | | · . | n in identification | Fitzgerald D., | | | | ional homology | | | | | monas aeruginosa PA | W., Lory S., Olson | R., Kas A., Larbig | gle W.O., Kowalik D gle W.O., Kowalik D | Stover C.K., Pham XQ.T., Erwin A.L., Mizoguchi S.D., Warrener | | | 45-2649(1984). | nd expression in Esche f Pseudomonas aerugino | ., harkills k.n | Harking D N | 26-53. | | division; Pseudomonadaceae | | | ADP-RIBOSYLTRANSFE | annotation undate) | | 638 AA. | | ALIGNMENTS | | | | | | | |
| Tragill | Arminjon F. | | | of s | | | | | vith glu | | | | | 01, an | X | K., Li | S., Y. | Warre | | | | scherichia | | 2: | | | adacea | | | RASE | | | | | | Q9k3c5 Q9k3c5 Q58081 | 318 | 446 | 873 242 | 085 | 471 | P14081 |
| ents of | · · · | | | equences | ί. | | | | lutamic | ת ח | | | | | | n R.M. | , Yuan Y., | ner P., | | | | coli of | | 7 | | | 10 | | | | | | | | | pseudomonas methanococc | bordetella | mycoplasma | arabidopsis rhodobacter | caenorhabdi | homo sapien | escherichia |

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"Crystal structure of the catalytic domain of pseudomonas exotoxin complexed with a nicotinamide adenine dinucleotide analog: implications for the activation process and for ADP ribosylation.";
Proc. Natl. Acad. Sci. U.S.A. 93:6902-6906(1996).
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           SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA
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e of Pseudomonas aeruginosa exotoxin domain III
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98.8%;
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Q99758; Q92
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Klugbauer N., Hofmann F.,
*Primary structure of a novel ABC
*Primary structure of a novel ABC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSPORTER
                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                 CHEMOTHERAPEUTICS DRUGS.

-! TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, FOLLOWED BY BRAIN, PANCREAS, SKELETAL MUSCLE AND HEART, WEARLY EXPRESSED IN PLACENTA, KIDNEY AND LIVER. ALSO EXPRESSED IN MEDULLARY THYROID CARCINOMA CELLS (MTC) AND IN C-CELL CARCINOMA.

-! DOMAIN: MULTIFUNCTIONAL POLYBEPTIDE WITH TWO HOMOLOGOUS HALVES, DOMAIN: MULTIFUNCTIONAL POLYBEPTIDE WITH TWO HOMOLOGOUS HALVES, EACH COUTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN ATP BINDING CASSETTE (ABC) DOMAIN (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE AIP-BINDING TRANSPORT PROTEIN FAMILY OF SIMILARITY: BELONGS TO THE AIP-BINDING TRANSPORT PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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MEDLINE=96326608; PubMed=8706931;
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                                                                                                      MIM; 601615;
                                                                                                                EMBL; U78735; AAC50967.1; EMBL; X97187; CAA65825.1;
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PS00211; ABC_TRANSPORTER;
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(Rel. 39, Last annotation update)
CASSETTE, SUB-FAMILY A, MEMBER 3 (ATP-BINDING CASSETTE
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.
Parsons J., Percy C., Rifken L., Ropora A., Sonnhammer D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
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STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
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                                                                                                                                                                                                                                                                                                                                                                         DNA REPLICATION LICENSING
                                                                     -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                              Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                             NCBI_TaxID-6239
                                                                                                                                                                                                                                                                                                                           Rhabditidae;
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                                                                                                                   .2 Mb of contiguous nucleotide sequence
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 non-profit institutions as long and this statement is not remove
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(Rel. 28, Last sequence update)
(Rel. 35, Last annotation update)
TION LICENSING FACTOR MCM6 HOMOLOG
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P -> S (IN REF. 2).
L -> P (IN REF. 2).
AF0098DAF7A04F5F (
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EMBL; 222181; CAA80357.1; J
EMBL; 222181; CAA80191.1; 
EMBL; 229095; CAA80191.1; J
WormPep; ZK632.1; CE00415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
SEQUENCE
                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast)
Eukaryota; Fungi; Ascomycota; Schizosaccharomy
Schizosaccharomycetales; Schizosaccharomy
                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 43.0 KDA PROTEIN C584.11C IN CHROMOSOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHPO
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PROSITE; PS0051; MCM_2; 1.

Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; DNA replication; Cell cycle; ATP-binding.

DOMAIN 346 554 MCM.

NP_BIND 397 404 ATP (POTENTIAL).
                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  Seeger K., Harris D., Wood V., Rajandream M.A., Barrell Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                           Q09885;
01-FEB-1996
Hypothetical SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                               SPCC584.11C.
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                               EMBL; AL032824; CAB37424.1;
                                                                                                                                                                                                                      STRAIN-972;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                Schizosaccharomyces.
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55; Conserv
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                                                                                                                                                                                                                                                                                         Ascomycota; Schizosaccharomycetaceae; etales; Schizosaccharomycetaceae;
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91130 MW;
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Pred. No. 3.3;
39; Mismatches
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 A65777B672310E68 CRC64;
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                                                                                                                                                                                                     Barrell B.
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                                                                                                                                                                                                                                                                                             TISSUE=Renal cell carcinoma;
MEDLINE=96279273; PubMed=866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING PROTEIN).
IL13RA2 OR IL13R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and characterization of a specific binding protein structurally related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caput D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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Henderson
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                                                                                             entities
or send a
                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97321053;
Guo J., Apiou F.,
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EMBL;
EMBL;
EMBL;
MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                         use
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                                                                                                                                                                                                                                                                                                                                                                                                  "Chromosome mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Biol. Chem. 271:16921-16926(1996).
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                                                                                                            ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buoppean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEATLFNETTF
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                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
                 X95302; CAA64617.1;
U70981; AAB17170.1;
Y08768; CAA70021.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.D., Whitters M.J., Fitz L., Neben S.L., O'Hara R.M. Jr., Turner K.J., (OCT-1996) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=8663118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9177784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.7%;
26.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89; DB Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lelias J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                          Lebeau B., Jacoon of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
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IL-5 receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                            Jacques Y., Minvielle
ıman interleukin-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T., Finnerty H., Wood C.R., Collidatabases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lefort S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INTERLEUKIN-13
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                                                                                                                                                                                                                                                                                                                                                     INTERLEUKIN-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collins
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RESULT 6
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Best Local
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SIGNAL 27 380
CHAIN 27 343
DOMAIN 27 343
TRANSMEM 344 363
DOMAIN 364 380
DISULFID 145 155
DISULFID 184 197
CARBOHYD 215 215
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Q10569;
Q1-OCT-1996 (Rel. 3
Q1-OCT-1996 (Rel. 3
Q1-OCT-1996 (Rel. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001777; -.
                                                        CHARACTERIZATION.

CHARACTERIZATION.

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EXECUTION: Service of the pre-many and polyadenylation factor CPF specifically interacts with releavage and polyadenylation factor CPF specifically interacts with the pre-many 3, processing signal AAUAAA.";

EMBO J. 10:4241-4249(1991).

EMBO J. 10:4241-4241-4241-4249(1991).

EMBO J. 10:4241-4241-4241-4249(1991).

EMBO J. 10:4241-4241-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLEAVAGE AND POLYADENYLATION
                                                                                                                                                                                                                                                                                                          Jenny A., Keller W.; "Jenny A., Keller W.; "Cloning of cDNAs encoding the 160 kDa subunit of the bovine cleavage "Cloning of cDNAs encoding the factor."; and polyadenylation specificity factor."; Nucleic Acids Res. 23:2629-2635(1995).
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95380277; PubMed=7651824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 KDA SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGK
STEP OF THE POLYADENYLATION REACTION.
SUBUNIT: CPSF IS A HETEROTETRAMER COMPOSED
SUBUNITS 160, 100, 70 AND 30 KDA.
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTTLVTATVENETYTLKTTNE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS01356;
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                                                                                                                                                                                                                                                                                                                                                                          Keller W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Bovine)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34, Last sequence update)
34, Last annotation update)
ADENYLATION SPECIFICITY FACTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata;
Cetartiodactyla; Ruminantia; Pec
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POTENTIAL.
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BY SIMILARITY.

BY SIMILARITY.

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Pred. No. 1.7;
26; Mismatches
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1.7;
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                                                    OF
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(POTENTIAL).
(POTENTIAL).
                                                      FOUR DISTINCT
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                                                                                               RNA RECOGNITION
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Best Local S
Matches 61
                                                                                                                                                                                                                           p14917;
p14917;
p14917;
01-APR-1990 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
UREASE BETA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROLASE).
UREB OR HPUB OR HP0072 OR JHP0067.
Helicobacter pylori (Campylobacter pylori), and
Helicobacter pylori J99 (Campylobacter pylori J99).
The proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by entitles requires a license approximate (See http://www.ior send an email to license@isb-sib.ch).
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between
the Euro
                                                                                                                       Labigne A., Cussac V., Courcoux P.;
"Shuttle Cloning and nucleotide sequences
genes responsible for urease activity.";
J. Bacteriol. 173:1920-1931(1991).
             Nucleic
                       "Nucleotide sequence of two for urease subunits."; Nucleic Acids Res. 18:362-36
                                                            MEDLINE-90221820; Put
Clayton C.L., Pallen
                                                                                                 SEQUENCE FROM
                                                                                                                                                                           MEDLINE-91161505; PubMed-2001995;
                                                                                                                                                                                                    SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; RNA-binding.
DOMAIN 894 909
 SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                    HELPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYGVALNSLTTGTTAFPLRTQEGVRITLDCAQAAFISYDKMVISLKGGEIYVLTLITDGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSFEVCDSILNIGPCANAAMGEPAFLSEEFQNSPEPDLEIVVCSGYGKNGALSVLQKSIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity 25.;
61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               524
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                                                            PubMed=2326167;
len M.J., Kleanthous H.,
                       18:362-362(1990)
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Pred. No. 12;
81; Mismatches
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PIR; S07885; URKCBP.
PIR; B38537; B38537.
PIR; B41502; B41502.
HSSP; P18314; 1FWE.
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SEQUENCE OF 1-20.
MEDCINE-90264448; PubMed-2188975;
MEDLINE-90264448; Perez-Perez
Dunn B.E., Campbell G.P., Perez-Perez
Dunn B.E., Campbell G.P., Perez-Perez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doi Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vov
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  Hydrolase;
METAL
METAL
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EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=90202165; PubMed=2318539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence comparison of two unrelated gastric pathogen Helicobacter pylori."; nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-J99
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MEDLINE=97394467; PubMed=92
                                                                         InterPro; IPR001924; ...
Pfam; PF00449; urease; 1.
PROSITE; PS00145; UREASE_2;
PROSITE; PS01120; UREASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Infect.
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CAPALYTIC ACTIVITY: UREA + H(2)O = CO(2) + 2 NH(3 COFACTOR: EACH CHAIN BINDS TWO NICKEL IONS. SUBUNIT: CONSIST OF TWO SUBUNITS (ALPHA AND BETA) SIMILARITY: BELONGS TO THE UREASE FAMILY.

CAUTION: IN HELICOBACTER THE BETA SUBUNIT IS WHAT
                                                                                                                                                                                                                                                                                                    L; M60398; AAA25021.1; -.

C; X17079; CAA34933.1; -.

C; A08818; CAA00811.1; -.

C; A07398; CAA0063.1; -.

C; AE000529; AAD07143.1; -.

C; AE001446; AAD05651.1; -.
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                                                                                                                                                                                HP0072;
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Metal-binding; Nickel
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138 138 NIC
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e from Helicobacter
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Best Local
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                                    X MEDILINE-94140354; PubMed-8307567;
X MAY DLX, Jessel M.T., Papamatheakis J.;
X Modi W.S., Furley J.A., Jessel M.T., Papamatheakis J.;
X Modi W.S., Furley J.A., Jessel M.T., Papamatheakis J.;
X MISCOLITON OF The CDNA and chromosomal localization of the gene
Y "Isolation of the duman axonal glycoprotein TAG-1.";
X Genomics 18:562-567(1993)
Y GENOMICS IN THE INITIAL GROWTH AND GUIDANCE CANONS.

AXONS. MAY BE INVOLVED IN CELL ADHESION.
Y GENOMICS INVOLVE
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CONFLICT
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Q02246;
Q1_JUL_1993 (Rel. 26, Create)
Q1_JUL_1993 (Rel. 26, Last s.
Q1_JUL_1999 (Rel. 38, Last a.
MXONIN -1 PARECURSOR (AXONAL G.
GLYCOPROTEIN 1).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                             MEDLINE=93145965; PubMed=8425542;
Hasler T.H., Rader C., Stoeckli E.T.,
"CDNA cloning, structural features, al
human TAG-1/axonin-1.";
Eur. J. Biochem. 211:329-339(1993).
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Catarrhini; Hominidae
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InterPro: IPR001777; -.
InterPro: IPR003006; -.
Pfam; PF00041; fn3; 4.
Pfam; PF00047; ig; 6.
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EMBL; X67734; CAA47963.1;
PIR; S28830; S28830.
MIM; 190197; T.
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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Best Local Similarity
Matches 65; Conser
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EMBL; Z29337; CAA82536.1;
PIR; S32777; S32777.
PIR; S44049; S44049.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleoprotein. SEQUENCE 695
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                                                                                                                                              Halobacterium volcanii (Haloferax volcanii)
Archaea; Euryarchaeota; Halobacteriales; Ha
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                      SEQUENCE FROM N.A.
MEDLINE=97474254; PubMed=9335278;
Kuo Y.-P., Thompson D.K., St Jean
                                                                                                                  Archaea; Euryarchaeota;
NCBI_TaxID=2246;
'Characterization of two l
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8 (Rel. 36, Last sequence SUBUNIT 1 (HEAT SHOCK)
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SHOCK PROTEIN CC
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34; Mismatches
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Haloferax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GGNDALKLAIDNALSI 91
                            R.L.,
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volcanii:
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                                                                                                                                                 Haloferax
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Marburg
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RESULT 11
VNUC_MABVM
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01-FEB-1996 (Rel. 3
01-FEB-1996 (Rel. 3
NUCLEOPROTEIN (NUCL
                                                                                                                                                                                                                                                           VNUC_MABVM
P27588;
01-AUG-1992
             J. Gen. virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00118; cpn60_TCP1; 1.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00750; TCP1_1; 1.
PROSITE; PS00751; TCP1_2; 1.
PROSITE; PS0095; TCP1_3; 1.
Chaperone; ATP-binding; Multigene family; Heat shock.
SEQUENCE 560 AA; 58925 MW; 88B73B2AD70DC341 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Bacteriol. 179:6318-6324(1997).
-i- FUNCTION: MOLECULAR CHAPERONE; BINDS U
VITRO, AND HAS A WEAK ATPASE ACTIVITY
-i- SUBUNIT: FORMS AN OLIGOMERIC COMPLEX C
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HSSP; P48424; 1ASX
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                                                        comparison to
                                                                  SEQUENCE FROM N.A.
MEDLINE=92166742; PubMed=1538192;
Sanchez A., Kiley M.P., Klenk H.D., Feldmann H.;
"Sequence analysis of the Marburg virus nucleoprotein
                                                                                                                                           NCBI_TaxID-33727;
                                                                                                                                                          Filovirus
                                                                                                                                                                                    Marburg
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REVISIONS
                                          viruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 LLAGGSSASAAEEAFDLWNECAKACVLDLK--DGVRSSRMSVDPAIADTNGQGVLHYSMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
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                                                                                                                                                                                       virus
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                                                                                                                                                                        SSRNA
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                                                                                                                                                                      (strain Musoke).
A negative-strand
                                                        Ebola
                                                                                                                                                                                                                  (NUCLEOCAPSID PROTEIN).
                            73:347-357(1992)
                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                         -GDGIDDMAQHY----
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Pred. No. 5
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                                                        negative-strand
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                                                                        gene:
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EMBL; Z12132; CAA78114.1; -
PIR; JQ1408; VHIWMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                               THIL_BACSU
005514;
30-MAY-2000
30-MAY-2000
30-MAY-2000
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SEQUENCE 69:
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
THIAMINE-MONOPHOSPHATE KINASE (EC 2.7.4.16) (THIAMINE-PHOSPHATE
                                                                                                                                                                                                                            Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                 the Bacillus subtilis chromosome.";
Microbiology 143:1861-1866(1997).
-i- CATALYTIC ACTIVITY: ATP + THIAM
                                                                                                                                                                                                                                                                         Bacillus subtilis
                                                                                                                                                                                                                                                                                                     KINASE).
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                                                                                                                                                        STRAIN=168 / MARBURG;
MEDLINE=97346038; PubMed=92
Sadaie Y., Yata K., Fujita
                                                                                                                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                            Ogasawara N.;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               341
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                                                                                                                             "Nucleotide sequence and analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ر.
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                                          PATHWAY: THIAMINE BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE THIAMINE-MONOPHOSPHATE KINASE FAMILY.
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                                                                       DIPHOSPHATE
                SWISS-PROT entry is
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65; Conserv
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    the
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                                                                                                                                                                                        MARBURG;
      Swiss
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                              PubMed=9202461;
., Fujita M., Sagai H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77456
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22.7%;
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us group; Bacillus.
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Pred. No. 7
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                                                                                          THIAMINE
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    ght. It is produced through a collaboration Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                               325
                                                                                           PHOSPHATE
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                                                                                             II
                                                                                                                                                                   Kasahara Y.,
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Matches 56
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EMBL; Z99107; CAB12409.1; -.
Subtilist; BG10693; thiL.
Thiamine biosynthesis; Transferase; Kinase.
SEQUENCE 325 AA; 35884 MW; 95D2D6762CFDBCCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   Q64632;
15-JUL-1998
15-JUL-1998
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAT
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
INTEGRIN BETA-4 PRECURSOR (GP150) (CD104).
between
the Europ
use by
                                                                                                                                                                                      Feltri M.L., Arona M., Scherer S.S., Wrabetz L.;
"Cloning and sequence of the cDNA encoding the beta 4 integrin subunit in rat peripheral nerve.";
Gene 186:299-304(1997).
                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY; TISSUE-Sciatic nerve; MEDLINE-97228432; PubMed-9074510;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ITB4_RAT
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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                                                                                                                                   -I- FUNCTION: INTEGRIN ALPHA-6/BETA-4 MAY MEDIATE ADHESIVE AND/OR MIGRATORY FUNCTIONS OF EPITHELIAL CELLS (BY SIMILARITY).
-I- SUBUNIT: DIMER OF AN ALPHA AND BETA SUBUNIT. BETA-4 ASSOCIATES WITH ALPHA-6 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231
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                                                                 SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
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                Swiss Institute of Bioinfo
Bioinformatics Institute.
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Rodentia;
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Pred. No.
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PF00362; integrin_B; 1.
S; PR00014; FNTYPEIII.
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                 PRECURSOR
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EGF_1; UNKNOWN_2.

EGF_2; UNKNOWN_2.

CG11 adhesion; Transmembrane; Glycoprocent adhesion; Glycoprocent adhesion; Transmembrane; Glycoprocent adhesion; Glycoprocent a
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Last annotation
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                                                                Created)
                                                                                                                                                                                                                                                         ----SDYTIGFGKFVDKVSVPQTDMRPEKLKEPWPNS----
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PIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.
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Pred. No. 43;
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CYTOPLASMIC (POTENTIAL).
CYSTEINE-RICH REPEATS.
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                (PENICILLINASE).
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"Role of the o.
structure of cl
Biochemistry 37
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                                                                                                                                                                                                                                                                                                                positive J. Biol.
                                                                                                           Herzberg
"Refined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-NCTC 9789; MEDLINE-91014696;
                                                                                      aureus PC1 at
J. Mol. Biol.
                                                                                                                                                                                                                 MEDLINE-87206177;
                                                                                                                                                                                                                                                                              SEQUENCE OF 25-28 MEDLINE-76135454;
                                                                                                                                                                                                                                                                                                                                 "Unique
                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence and Staphylococcus aureus plasubtilis, and Staphylococ
                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM PLASMID-p1258,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NCTC 9789; TRANSPOSON=Tn552; MEDLINE-91014696; PubMed=2170815; Rowland S.J., Dyke K.G.H.; Th552, a novel transposable element Mol. Microbiol. 4:961-975(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gillspie M.T., Skurray R.A.;
"Nucleotide sequence of the blaz gene
beta-lactamase transposon Tn4002.";
Nucleic Acids Res. 17:8854-8854(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SK456; TRANSPOSON=Tn4002; MEDLINE=90067850; PubMed=2555777;
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STRAIN=PC-1; PLASMID=p1258;
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                                                                                                                                                              Science
                                                                                                                                                                                                        Herzberg O.,
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                                                                                                                                                                                                                                                                       Ambler R.P.;
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                                                                                                                                                                                                                                                                                                                                                       MEDLINE-82030947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87165797;
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                                                                                                                                                                                              "Bacterial resistance
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                                                                   -RAY CRYSTALLOGRAPHY
                                                                                                                                                                                    beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                     Dillis, and Staphylococcus aureus. Bacteriol. 169:1763-1766(1987).
                                                                                                                                                                                                                                                          amino
                                                                                                                                          CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                             lin J.R., Murray C.L., Rabinowitz J.C.; features in the ribosome binding site sequence staphylococcus aureus beta-lactamase gene."; Chem. 256:11283-11291(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p1258
                                                                                                                                                              236:694-701(1987).
                                                                                      crystal structure of beta-lactamase
Cl at 2.0-A resolution.";
Biol. 217:701-719(1991).
                                                                                                                      0:
                                                                                                                                                                                                                                                 acid sequence of S
. 151:197-218(1975)
                                                                                                                                                                                                                                                                      25-281.
35454; PubMed=1218078;
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               Pieper U., Kapadia G., Pannell L.K., Fomega-loop in the activity, substrate class A beta-lactamase.";
37:3286-3296(1998).
                                                                                                                                                                                                        Moult
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PubMed=3107125;
                                                       PubMed=9521648;
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PubMed=2005620;
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EMBL; X16471; CAA34491.1; ...
EMBL; X1526; AAA982391; ...
EMBL; X52734; CAA36953.1; ...
PIR; A01002; PNSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen C.C., Herzberg O.; "Relocation of the catalytic carboxylate group in class A beta-lactamase: the structure and function of the mutant enzyme Glu166->Gln:AsnI/O--Asp."; Protein Eng. 12:573-579(1999).

-i- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)O = A SUBSTITUTED E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE=99365425; PubMed=10436083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY
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S06757;
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1KGG;
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o; IPRO01466; -.
pr00144; beta-lactamase; 1.
pr00118; BLACTAMASEA.
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30-JAN-94.
31-AUG-94.
31-APR-94.
26-SEP-97.
12-MAR-97.
12-MAR-97.
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28-MAY-99.
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                                                                                                                                                                                                                                                                                                                                                                           BETA-LACTAMASE
                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure;
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                                                         "The control region of the pdu/cob typhimurium.";
                                                                                                                                         Salmonella typhimurium
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MEDLINE=98012959; pubMed=9352910; Bobik T.A., Xu Y., Jeter R.M., Otto K.E., Roth J.R.; Bobik T.A., Xu Y., Jeter R.M., Otto K.E., Roth J.R.; Propanediol utilization genes (pdu) of Salmonella t genes for the propanediol dehydratase.";
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                          Salmonella.
                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                  NCBI_TaxID=602;
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(Rel. 30, Last sequence update)
(Rel. 39, Last annotation update)
UTILIZATION PROTEIN PDUB.
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                                                       176:5474-5482(1994).
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                                                                                                                                   gamma subdivision; Enterobacteriaceae;
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF026270; AAB84106.1; -. StyGene; SG10279; pduB. SEQUENCE 233 AA; 24015 MW; 2EE1E58C0075F29E CRC64;
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                                                                                                      191 EAILVISGDS 200
                                                                                                                                                 165 ELLAKLARDA 174
                                                                                                                                                                                         132 -ARASYALEKAFGAPIGRACGIIVGAPASVGVLMADTALKSANVEVVAYSSPAHGTSFSN 190
                                                                                                                                                                                                                                   117 QARGSWSLN--WLVPIGHE-----KPSNIKVFIHE--LNAGN--QLSHMSPIYTIEMGD 164
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                                                                                                                                                                                                                                                                                                      66 -----GVLHYSMVLEGGNDA--LKLAIDNALSITSDGLTIRLEGGVEPNKP--VRYSYTR 116
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Q18466 homo sapien
Q9355w4 helicobacte
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
|--------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|-------------------|--------------------|-------------------|
| 82.5 | 82.5 | 82.5 | 83 | 83 | 83 | 83 | 83 | 83.5 | 83.5 | 83.5 | 84 | 84 | 84 | 84.5 | 84.5 | 84.5 | 84.5 | 85 | 85 | 85 | 85.5 | 85.5 | 85.5 | 85.5 | 86 |
| 6.2 | 6.2 | 6.2 | 6.3 | 6.3 | 6.3 | 6.3 | 6. ₃ | 6.ω | 6.3 | 6.3 | 6.3 | 6.3 | 6. ₃ | 6.4 | 6.4 | 6.4 | 6.4 | 6.4 | 6.4 | 6.4 | 6.5 | 6.5 | 6. 5 | 6.5 | 6.5 |
| 425 | 410 | 344 | 9376 | 1150 | 921 | 351 | 220 | 442 | 406 | 344 | 984 | 685 | 681 | 4587 | 3729 | 559 | 220 | 856 | 856 | 441 | 2276 | 2055 | 859 | 408 | 701 |
| ν | 5 | 2 | N | 2 | ω | 10 | N | N | ν | 2 | N | N | 10 | 11 | ν | 10 | ນ | 14 | 14 | ນ | 5 | 11 | 14 | 2 | σ |
| Q9XCP9 | Q9NGP6 | Q916T5 | 085168 | Q9K9M0 | Q9HE41 | Q9LRZ4 | Q9ZNC4 | 034974 | Q9L015 | Q9RJR6 | Q9XBJ1 | P95597 | Q9LV16 | Q9QXA3 | 033956 | 023409 | Q9R7J7. | Q70200 | Q71014 | P72763 | Q9TXQ1 | Q9Z1K3 | Q9Q072 | Q9LA06 | Q24713 |
| | Q9ngp6 mastigamoeb | Q916t5 pseudomonas | O85168 pseudomonas | Q9k9m0 bacillus ha | Q9he41 neurospora | Q9lrz4 arabidopsis | Q9znc4 helicobacte | 034974 bacillus su | Q91015 streptomyce | Q9rjr6 streptomyce | Q9xbj1 bacillus ce | P95597 rhizobium e | Q9lv16 arabidopsis | Q9qxa3 mus musculu | 033956 streptomyce | 023409 arabidopsis | Q9r7j7 helicobacte | Q70200 human immun | Q71014 human immun | | Q9txq1 caenorhabdi | Q9z1k3 mus musculu | Q9q072 chimpanzee | Q91a06 lactococcus | Q24713 drosophila |

ALIGNMENTS

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V1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 44.1 KDA PROTEIN.
SCF51.09C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9RJS6;
                    Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map the 8 mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
Mol. Microbiol. 21:77-96(1996).
EMBL; AL132707; CAB59707.1; -.
InterPro; IPR002504; -.
InterPro; IPR002504; -.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
                                                                                                                                                                                                   STRAIN=A3(2);
Cerdeno A.M., Parkhii
Submitted (OCT-1999)
                                                                                                                                                                                                                                                                                                                                Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                   Seeger K.J., Harris D.;
Submitted (OCT-1999) to
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Hypothetical protein. SEQUENCE 416 AA; 4
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                , Parkhill J., Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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MW;
                                                                                                                                                                                                    Barrell B.G., Rajandream M.A.;
EMBL/GenBank/DDBJ databases.
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F57F8BFEE3B54207 CRC64;
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Query Match

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Дb
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Best Local S
Matches 50
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MEDLINE-20437337; pubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Lagrou M. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Hickey M.J., Brinkman F.S.L., Tolentino E., Westbrock-Wadman S., Yuan Y., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PA01, an "poportunistic pathogen."; Nature 406:959-964(2000).

EMBL; AE004504; AAG04079.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL PROTEIN PA0690
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                                                                                                                                                                                                                                                                                                                              Interpro; IPR001969; -.
PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 4180 AA; 430016 MW; EB181EA3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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3317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLEKLSRDRQISVGVYI----AGRLLASYS-----ADALLVATPTGSTAYSFAAGGPV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V--PIGHEKPSNIKVFIHELNAGNQLSHMSPTYTIEMGDELLAKLARDATFFVRAHESNE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLTLRASRLLEIPAEMEALLRY-----GRGPLLPPPRVRTDCESGDEWGIALNVTALNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTLGGDGTFLRGARLAAENDALILGVDLGRVGFLTEVPAPAVRSALDAVRDGGLEPESRM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IERVGLVVHGGREGAAEAAREVREWCDENAVACTDIDVWSDTGRHSAREEVDAAGDPDLV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSPRAEALVFTAVAPHMTFDRSVVTAPDEPVGLRILERSGRAAVSIDGQLRGVLDPGDWL 339
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                                                                                                                                      LKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDG-------
  DLNVRIGGEVNPSREARATQTYSSSG---FDGLYSGG----
                                                -LTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL-NAGNQLSH 153
                                                                                                   LGGGNLSMRTGGDAGNIAPRGDGSIPSSGNLNPRSQGLVLAVAGTGRLTSDGALQLGGGG
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75; Conserv
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27.8%;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                  Score 93.5;
Pred. No. 58;
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annotation
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Best Local S
Matches 42
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01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanahashi T., Kita M., Kodama T., Sawai N., Yamaoka Y., Mitsufuj
Katoh F., Kashima K., Imanishi J.;
"Comparison of PCR-restriction fragment length polymorphism and
direct sequencing method for differentiating Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision;
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                                                                                                                 Q9DDT1;
01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00449; urease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01120; UREASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD002467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P18314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB028036;
                                                  Brachydanio rerio (Zebrafish) (Zebra danio)
Eukaryota; Metazoa; Chordata; Craniata; Ver
Actinopterygii; Neopterygii; Teleostei; Eut
Cypriniformes; Cyprinidae; Rasborinae; Dani
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  Yoder J.A., Lit
                       SEQUENCE FROM N.A.
                                        NCBI_TaxID=7955;
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42; Conserv
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                                                         Rasborinae; Danio
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EMBL; AF295372; AASEQUENCE 1180 AA
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01-NOV-1996
01-NOV-1996
01-NOV-1998
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EMBL; X67865; CAA48050.1; -.

EMBL; X67865; CAA48050.1; -.
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Lambda phage group.
NCBI_TaxID=10724;
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     <del>-</del>
                    ELLAKLARDATFFVRAHESNEMQPTLAISHA
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35; Conserv
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Pred. No. 2.2;
21; Mismatches
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Q28733; Q28736;
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Mueller-Seitz M., Kaupmann K., Labeit S., Jockusch
"Chromosomal localization of the mouse titin gene
"muscular dystrophy with myositis' and nebulin gen
2.";
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Mammalia; Eutheria;
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                           YSYTROARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNOLSHMSPIYTIEMGDELLAKLA 171
                                                                                                                                                                                                                                                                                                                                             DAAIIDVTSS---FTSLVLDNVNRYDSGKYTLTLENSSGTKSAFVTVRVLD--TPSPPVN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELISHIVQGEHYFWNNHFSANIPPTASDSDA
                                                                                                                                                                                                               EGCSYYFRVTAENEYGIGLAARTADPIKVAEVPQPPGKITVDDVTRNSVSLSWTKPEHDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat
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Metazoa; Cl
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531 AA;
 5 (TrEMBLrel.
5 (TrEMBLrel.
1 (TrEMBLrel.
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                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; fn3; 3.
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58437
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Rodentia;
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Pred. No. 5
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Sciurognathi;
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! titin.";
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thi; Muridae; Murinae; Mus
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ion update)
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Matches
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Interpro; IPR001777; -.
Interpro; IPR003006; -.
Interpro; IPR003006; -.
Pfam; PF00041; fn3; 50.
Pfam; PF00047; ig; 15.
PRINTS; PR00014; FNTYPEII
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Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=9023853; PubMed=2129545; Labeit S., Barlow D.P., Gautel M., Francke U., Leonard K., Wardale J., "A regular pattern of two types of of titin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Labeit S., Gautel M., Lakey A., Tr: "Towards a molecular understanding EMBO J. 11:1711-1716(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X64696; CAA45937.1;
EMBL; X17329; CAA35207.1;
HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 4305-5320 FROM N.A. TISSUE=PSOAS MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92258380; PubMed=1582406; Labeit S., Gautel M., Lakey A., T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-6805 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CE12;
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 345:273-276(1990).
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  Q10466 PRELIMINARY; PRT; 26926 AA.
Q10466;
Q10466;
Q104066;
Q10406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPAIADTNGOGVLHYSMVLEGGN--DALK--LAIDNALSITSDGLTIRLEGGVEPNKPVR 111
                                                                                                                                                                                                                                                                                                                                                                               LKYTEITKDSVSITWEPPL-LDGGSKIKNYIVEKRDSTRKSYAAVVTNCHKSSWKIDQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                     YSYTROARGSWSLUWLVPIGHEKPSNIKVFIHELNAGNOLSHMSPIYTIEMGDELLAKLA 171
                                                                                                                                                                                                                                                    VSVV----MAQTQPRREKRWSEWASGKVL
                                                                                                                                                                                                             GSKIIQYIVEMQAKHSEKWSECARVKSL 5118
                                                                                                                                                                                                                                                                                                EGCSYYFRVTAENEYGIGLPARTADPIKVAEVPQPPGKITYDDVTRNSVSLSWTKPEHDG
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6875
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nilarity 22.1%;
Conservative 3:
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5 AA;
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; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              759127 MW;
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                                                                                                               PRT;
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ing of titin.";
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3.3e+02;
79;
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motif
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the
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PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0726; LEXASSEPTASE.
PROSTE; PSO0933; FGGY_KINASES_1; UNKNOWN_1.
PROSITE; PSO0038; HELIX_LOOP_HELIX; UNKNOWN_1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
PROSITE; PS000435; PEROXIDASE_1; UNKNOWN_1.
PROSITE; PS000435; PEROXIDASE_1; UNKNOWN_1.
PROSITE; PS00010; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
SMART; SM00408; IGC2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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EMBL; X64697; C
EMBL; X90568; C
EMBL; X64699; C
HSSP; P56276; 1
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"Titins: giant proteins in charge of elasticity.";
                                                                                                                                                                                         Interpro; IPRO00129; ...
Interpro; IPRO00577; ...
Interpro; IPR000577; ...
Interpro; IPR000719; ...
Interpro; IPR000719; ...
Interpro; IPR001745; ...
Interpro; IPR001777; ...
Interpro; IPR002016; ...
Interpro; IPR003015; ...
Interpro; IPR003015; ...
Interpro; IPR003015; ...
Interpro; IPR00359; ...
Interpro; IPR00359; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Labeit S., Gautel M., Lakey A., Tr. "Towards a molecular understanding EMBO J. 11:1711-1716(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 22277-25376 FROM MEDLINE=92258380; PubMed=1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1976-2014 FROM Labeit S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95331314; PubMed=7607248; Gautel M., Castiglione-Morelli M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1994) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         titin kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A calmodulin-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                            +
                                                                                                                                                             Pfam; PF00041; fn3; 132.
Pfam; PF00047; ig; 95.
Muscle protein; Cytoskereton; Serine/threonine-protein kinase;
                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THIS GIANT MUSCLE PROTEIN MAY BE INVOLVED IN MUSCLE ASSEMBLY AND IN MAINTAINING THE STRUCTURAL INTEGRITY OF SARCOMERES. MAY HAVE PROPEIN KINASE ACTIVITY.

SARTOMERES. MAY HAVE PROPEIN KINASE ACTIVITY.

SALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE DISTRIBUTION. DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHIN AN ONE TISSUE. THE SEQUENCE SHOWN HERE IS THAT OF THE HEART ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N2-B.
TISSUE SPECIFICITY:
SIMILARITY: TO THE (
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO IMMUNOGLOBULIN C2-LIKE
                                                                                                                                                                                                                                                                                                                                                                                      X64698; CAA45939.
X83270; CAA58243.
                                                                                                                                                    PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270:293-296(1995).
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                                                                                                                                                                                                                                                                                                                                                              CAA45938.
CAA62188.
                                                                                                                                                                                                                                                                                                                                     TILK
                                                                                                                                                                                                                                                                                                                                                   CAA45940
                                                                                                                                                    pkinase; 1.
 Cytoskeleton; Structural protein; Calmostroperotein kinase; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=7569978;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMUNOGLOBULIN SUPERFAMILY.
DOMAINS AND 132 FIBRONECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
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e C-terminus of J
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                       Calmodulin-binding;
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TYPE III-LIKE
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Fayello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Forntians B., Walkinson-Sproat J., Wohldman P.;
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Rhabditidae; Peloderinae; Caer
NCBI_TaxID=6239;
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EMBL; 278542; CAB01748.1; -.
SEQUENCE 915 AA; 104584 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                   6 HWIPL------AEEAFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMGDELLAKLARDATFFVRAHESNEMQPTLAISHA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DMQDGVKNN-LSVGPATEAGDGEGLI----VTAGGIDTHSHFISPQQIPTAFASGVTTMI 82
                                                                                                                                                                                                                                                  -----WN----ECAKACYLDLKDGYRS-SRMSYDPAI-ADTNGQGVL--HYSMVLEGGNDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTGPADGT - - NATTITPGRRNLKWMLRAAEEYSMNLG - FLAKGNASNDAS - - - - -
AESDNESLAHELNMLNAASMSENQLSDDELVNNVKLDTLFNYKNPKSANTFLAPYKCAKK
                                               KPSNIKVFIHELN-----AGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEM
                                                                                                 QKLTINSASEVKIGKHAETEDSGT
                                                                                                                                                   LKLAIDNALSI - - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                        69;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contiguous nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                             6.7%;
22.7%;
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25.2%;
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                                                                                                                                                -TSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                     47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 88.5;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OAEAFA63A58F8566 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence from chromosome
                                                                                                 - NGPMPPALMK
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19;
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                                                                                                                                                                                                                                                                                                                                                                                                     96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 915
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QY
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RESULT 12
O48490
ID O48490
AC O48490;
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                                                                                                                                        밁
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Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001882; ...
InterPro; IPR003379; ...
InterPro; IPR003379; ...
Pfam; PF00289; CPSase_L_chain; 1
Pfam; PF00364; biottin_lipoy1; 1.
Pfam; PF00682; HMGL-like; 1.
Pfam; PF02436; PYC_OADA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q16921;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 16,
Q1-MAR-2001 (TrEMBLrel. 16,
PYRUVATE CARBOXYLASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q16921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Biochemical, molecular, and phylogenetic analysis of pyruvate carboxylase in the yellow fever mosquito, Aedes aegypti."; Insect Biochem. Mol. Biol. 27:133-147(1997).

1 - COFACTOR: BIOTIN (BY SIMILARITY).

EMBL: L36530; AAB64306.1;

HSSP: P10802, 1IYU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aedes aegypti (Yellowfever mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=97218699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
    048490
048490;
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                                                                                                                                                                                                                                                                                                                                                                                                           697
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                                                                                                                                                                                                                                                                                                                       752
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                                                                                                                                                                                                                                                                                                                                                                40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MHLIPHWIPLVASLGLLAGGSSASAAEEAF-----
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                                                                                                                                                                                                                                                                                                                                                                                                         LNYLPNLI----LGMEAAGNAGGVVEAAISYTGDVSDPTKKKYDLKYYTNLADELVKAG 751
                                                                                                                                                                                                                                                                                                                  THILCIKDMAGLLKPQAAKLLIAAIREKHPDVPIHIHTHDTSGAGVASMLACAEAGADVV
                                                                                                                                                                                                                                                                                                                                                           ----CVLDLKD------GVRSSRMSVDPAI--ADTNGQGVLHYSMVLEGGNDAL 81
                                                                                                                                                                                                                            DVAVDSMSGMTSQPSMGAVVASLQGTPLDTGLNLRDISEYSAYWEQTRTLYA-----PFE
                                                                                                                                      CTTTMKSGNADVYLNEIPGGQYTNLQFQAYSLGLGDFFEDVKKAYREANLLL
                                                                                                                                                                               --GHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGD--ELLAKLARDATFFV
                                                                                                                                                                                                                                                         KLAIDNALSITSD---GLTIR-----LEGGVEPNKPVRYS-YTRQARGSWSLNWLVPI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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IPR000891; -.
IPR000901; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=9066123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132201 MW; D4F583138D49BFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
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Pred.
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                      311
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                                        A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------DLWNECAKA- 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1195
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                                                                                                                                                           918
                                                                                                                                                                                                    178
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Q29117
ID 229
AC 029
DT 01-1
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Best Local :
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
COMPLETE NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Alonso J.C., Luder G., Stiege A.C., Chai S., W
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ
EMBL; X97918; CA66538.1; -.
SEQUENCE 311 AA; 35943 MW; 1BD3468DA07DAF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriophage SPP1.
Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lambda phage group.
NCBI_TaxID=10724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q29117; Q29033; Q29034;
Q29117; Q29033; Q29034;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-MAR-2001 (TrEMBLrel. 16,
                               InterPro; IPR001777; ...
InterPro; IPR003006; ...
InterPro; IPR003006; ...
InterPro; IPR003008; ...
Pfam; PF00041; fn3; 3.
Pfam; PF00041; fn3; 3.
Pfam; PF00041; ISYTYPEIII.
SMART; SM00408; IGC2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93365278; PubMed-8359022; Fritz J.D., Wolff J.A., Greaser M.L.; "Characterization of a partial cDNA clone encoding porcine skeletal muscle titin: comparison with rabbit and mouse skeletal muscle titin: emparison with rabbit and mouse skeletal muscle titin sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                         Tanabe R., Muroya S., Nakajima I., Chikuni K., Tanabe R., Muroya S., Nakajima I., Chikuni K., Tanabe R., Muroya S., Nakajima I., Chikuni K., "Skeletal muscle connectin primary structures species and muscle type.";

J. Food Sci. 62:461-461(1997).

J. FOOD SCI. 62:461-461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comp.
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                                                                                                                                                                                       EMBL; M97767; AAA02948.1;
EMBL; D85840; BAA12876.1;
EMBL; D85841; BAA12877.1;
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-MUSCLE;
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                            SMART; SM00408; IGC2;
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23.2%;
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Last sequence update)
Last annotation update)
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as related
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Sus.
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Best Local Similarity
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NON_TER
SEQUENCE
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Li J., Kremenetskaia I., Luros J., Araujo R., Au M., Bredel V
Buehler E., Conway A., Dewar K., Feng J., Kim C., Kurtz D., L
Palm C., Shinn P., Sun H., Davis R., Ecker J., Federspiel N.,
                                                                                                                                                                                                                                                                                                                        STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R.,
                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
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F13M7.9.
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                                            SEQUENCE 1064 AA; 119675 MW; SCUDENTING MAR 2000); AAR40445.1; -. Interpro; IPRO01296; -. Pfam; PF00534; Glycos_transf_1; SEQUENCE 1064 AA; 119675 MW;
                                                                                                              STRAIN-CV. COLUMBIA;
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STRAIN-CV. COLUMBIA;
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STRAIN-CV. COLUMBIA;
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itted (JUN-1998)
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                                                                                                                                              (AUG-1998)
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Bredel V.,
urtz D., Li Y.,
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PE PROSITE; PS01120; UREASE_1; 1

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SEQUENCE 220
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Q9WXL2;
01-NOV-1999
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HSSP; P18314; IFWB.
InterPro-
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Tanahashi T., Kita M., Imanishi J.;
Katoh F., Kashima K., Imanishi J.;
"Comparison of PCR-restriction fragment lengt
"Comparison of properties of differentiating
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Tanahashi T.,
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KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; KW IL-IR; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria; KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection; KW graft verses host disease; sepsis; inflammation; allergy; XX Ax autoimmune dysfunction.

XX Homo sapiens.

XX FH Key Location/Qualifiers
FT Peptide /note= "Signal peptide"
FT Protein /note= "Signal peptide"
FT Region /note= "Mature hII-IR"
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N-PSDB; AAQ49933.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New fusion protein tumour necrosis factor and human interleukin-l receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
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                                                                                                                                                                                                            Human interleukin-1 receptor; IL-1R; human
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                                                                                                                                                                                                                                                                                              AAP92001;
30-APR-1984;
21-DEC-1984;
                                                                                                                         Region
                                                                                                                                          Protein
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                       Derived sequence of
                                          24-NOV-1988;
                                                                      31-MAY-1989
                                                                                                 EP381296-A.
                                                                                                                                                                                                                                                                                                                                                                                           :||||| :|| |
322 migicvtltvii 333
                                                                                                                                                                                                                                                                                                                                                                                                                        1 LIGICVAVTVAI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNF-R-linker-TNF-R-linker-TNF-R or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                     (first entry)
 84US-0605540
84US-0684560
                                           88EP-0311150
                                                                                                                           Location/Qualifiers
18
337..356
                                                                                                                                                                                                                                          human interleukin-1 receptor (IL-1R) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                   T-cell line clone 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT
AAP90330
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SON COCCCXX B XX PTT DDR XX PX XX PX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75:
Best Local Similarity 66.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA coding for mammalian interleukin-receptor - used for obtaining protein and antibodies for diagnosis and therapy involving immune or inflammatory activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Derived sequence of the coding region of a cDNA encoding human IL-IR. The Protein feature = N-terminus of mature protein. The Region feature = transmembrane region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dower SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; figure 5A-5C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN90118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMMU-) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone; interleukin-1 receptor; human; immune regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1989 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP90330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP90330 standard; protein;
                                                                                                                                                                                                              DNA sequences encoding mammalian interleukin-1 receptors used to regulate immuno or inflammatory responses or detect IL-1 and its receptor interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human interleukin-1 receptor
                                                                    Peptide of human interleukin-1 receptor (see AAN90031). This is used in human and veterinary medicine to regulate or inflammatory responses, and to detect and study IL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W08904838-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine
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                                                                                                                                                                                                                                                                                                                     N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 migicvtltvii 349
                                                                                                                                                                                                                                                                                                                                              WPI; 1989-178365/24.
                                                                                                                                                                                                                                                                                                                                                                                       Dower SK,
  Sequence
                                                   molecules and their receptors
                                                                                                                                                                     Disclosure; Table 4a-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LIGICVAVTVAI 12 :||||| :|| |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                     AAN90031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569 AA;
                                                                                                                                                                                                                                                                                                                                                                                            March CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87US-0258756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88WO-US03926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sims
                                                                                                                                                                                                                                                                                                                                                                                               Sims
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32pp; English
                                                                                                                                                                             51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JE,
                                                                                                                                                                                                                                                                                                                                                                                               JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42;
Pred. No.
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15;
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Best Local Similarity
Whiches 8; Conserv:
        This protein is the soluble human interleukin-1 receptor (IL-IR). by mutating codon 336 (AAG) of the CDNA encoding IL-IR (AAQ71901), to form a stop codon (TAG) a truncated receptor, comprising the extracellular domain only, is generated. This truncated receptor retains its ability to bind interleukin-1 but is released extracellularly and therefore is inactive in signal transduction. The methods of the invention are useful for preventing the development of arthritis and for therapeutic use, eg. for repairing and regenerating the connective tissue. The gene is also useful in a compound for parenteral administration for prophylaxis or treatment. (Also see AAR59091 for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human interleukin-1 receptor
                                                                                                                                                                                                                                                                                                                      07-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human interleukin-1 receptor; I1-1R; truncated; connective tissue; prevention; arthritis; therapy; repairing; regenerating; ligament; tendon; cartilage; synovium; prophylaxis; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR59090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR59090 standard;
                                                                                                                                                                     Methods for introducing genes into connective tissue treating connective tissue disorders, e.g. arthritis
                                                                                                                                                                                                                                                                                              08-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                       WO9420517-A
                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                         N-PSDB; AAQ71901
                                                                                                                                                                                                                                                                     (UYPI-) UNIV PITTSBURGH
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                                                                                                                                                                                                                       1994-302952/37
                                                                                                                                             Page 49-51; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                             Evans CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                              93US-0027750
                                                                                                                                                                                                                                                                                                                      94WO-US02414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142..196
248..312
                                                                                                                                                                                                                                                                                                                                                                                                          336..356
/note= "transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "a truncated receptor
    mutation of the codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                             Glorioso
                                                                                                                                                                                                                                                                                                                                                                                              "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                           to a stop codon"
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Pred.
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Query Match
Best Local Similarity
"~+~hes 8; Conserv
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              The amino acid sequence of the human interleukin-1 (IL-1) receptor (IL-1R) encoded by the insert fragment R3A. The gene (AAQ73764) encodes CC a 65 kD protein precursor which is converted to 63.5 kD protein. The CC protein then undergoes glycosylation to produce a protein of around CC 82 kD. The gene was isolated from a cDNA library, derived from RNA from CC a human T-cell line (designated clone 22), by using a probe prepared CC from the murine IL-1R gene sequence (AAQ73762). Nine positive clones CC complete coding region of the human IL-1R. The purified IL-1 receptor, CC as part of compositions, can be used for the diagnosis of IL-1 or its CC receptors. The receptor will also be useful for the production of CC antibodies used in diagnosis and therapy. In addition, the purified IL-1, CC thereby providing means for regulating the immune or inflammatory CC activities of IL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine; interleukin-1; receptor; glycoprotein; human; IL-1-alpha; expression vector; antibody; diagnosis; therapy; IL-1; IL-1R regulation; regulate; immune; inflammatory; activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant cell lines expressing interleukin-1 receptor proteins - also antibodies and compositions for use in diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-343308/43.
N-PSDB; AAQ73764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1987;
25-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 5; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human IL-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          March CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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88US-0160550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 18..569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urdal DL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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QS

Sequence

569

AA;

Query Match Best Local Matches

Similarity 8; Conserv

Conservative

2;

Mismatches

75 66

5.7%;

Score 42; DB Pred. No. 15;

15; 2

Length 569; Indels

0;

Gaps

0

RESULT AAR90376

σ

AAR90376 standard;

protein;

569 AA

AAR90376;

22-JUL-1996

(first entry)

receptor

I-type

Human interleukin-1 Human interleukin-1

in-1 receptor I-type; bone resorption inhibitor; metabolic disease; osteoporosis; hypercalcaemia

bone

QΥ B

1 LIGICVAVTVAI 12 :||||| :|| | 338 migicvtltvii 349

0

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Human interleukin-l receptor I-type (IL-IR) preferably comprises of amino acids 1-319, and more preferably is a soluble protein comprising of amino acids 1-312. It is useful as a bone resorption inhibitor and can be administered intravenously or intramuscularly. A pharmaceutical composition, containing IL-IR as an active ingredient, helps prevent and treat metabolic diseases of the bone matrix which are caused by the abnormal decrease of calcium and bone matrix in the bone, e.g. osteoporosis and hypercalcaemia. The IL-IR is a superior therapeutic agent to the prior art medications giving a more satisfactory effect for metabolic bone diseases caused by abnormal bone resorption by inactivating osteoclasts. Bone resorption inhibitory activity of the protein has been proved by assaving a direct action on osteoclast activity.
                                                                                                                                                                                                                              Composition contg. interleukin-1 receptor, or soluble fragment treating and prophylaxis of metabolic bone diseases e.g. osteoporosis or hypercalcemia.
                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            17-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                     12-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP687470-A2
                                                                                                                                                                                                                                                                                     WPI; 1996-041308/05
                                                                                                                                                                                                                                                                                                             Katoh M,
                                                                                                                                                                                                                                                                                                                                    (FARH ) HOECHST JAPAN LTD. (FARH ) HOECHST JAPAN KK.
                                                                                                                                                                                                           Claim
                        assaying a direct action on
           formation assay
                                                                                                                                                                                                         5; Page 5-7; 10pp; English
                                                                                                                                                                                                                                                                                                              Kitamura K;
                                                                                                                                                                                                                                                                                                                                                                              94JP-0135275
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21..33
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21..569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "signal peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "soluble protein shuIL-1R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "soluble protein"
                             osteoclast
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Query Match

75.0%;

Score 42;

DВ

18;

Length 569;

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AAW06541
AAW06541
AAW06X
XX AAW0
XX AAW0
XX Int
XX Int
KW Syno
KW Syno
KW Gen
XX Key
FH Pep
FT Pep
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FT Pro
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-1 receptor; IL-1R; (
synoviocyte; connective tissue; 
gene therapy; retrovirus.
                      The human interleukin-1 receptor (IL-IR) (AAW06541) amino acid sequence can be deduced from a cDNA clone (AAT45876) isolated from a sequence can be deduced from a cDNA clone (AAT45876) isolated from a human T-cell cDNA library. cDNA encoding the extracellular IL-1 binding domain of IL-IR can be generated by PCR (see also AAT45878-79) and incorporated into a retrovirus vector subsequently used to transfect a packaging cell line. Viral particles are produced that can be used to infect synovial cells in culture. Infected cells are then transplanted into the damaged cartilage of a patient. Soluble IL-IR is expressed that binds to and neutralises IL-1 in vivo, preventing degradation of cartilage, as a means of treating arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW06541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW06541 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human interleukin-1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                               Treatment of a mammalian cartilage defect e.g. arthritis - by re-implanting chondrocyte(s) and synoviocyte(s) contg. DNA encoding a protein to inhibit interleukin-l associated cartilage damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 migicvtltvii 349
                                                                                                                                                                                                                                                                     WPI; 1997-042874/04.
N-PSDB; AAT45876.
                                                                                                                                                                                                                                                                                                             Evans CH, Glorioso
                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9639196-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                      Disclosure; Page 77-79; 112pp; English.
                                                                                                                                                                                                                                                                                                                                     (UYPI-) UNIV PITTSBURGH
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LIGICVAVTVAI 12
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8; Conserv
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1..17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%;
66.7%;
                                                                                                                                                                                                                                                                                                              JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366
                                                                                                                                                                                                                                                                                                                Kang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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Pred. No.
                                                                                                                                                                                                                                                                                                                В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cartilage; knee joint; chondrocyte;
; inflammation; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                   Robbins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                   PD;
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RESULT
AAB37791
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                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is given in a specification relating to novel compositions and methods containing tetracycline or tetracycline-like compounds for treating and/or preventing acute inflammatory responses a diseases. Such diseases include acute inflammatory conditions associate with viral haemorrhagic diseases (including diseases caused by Bunyaviridea, Filoviridae, Flaviviridae or Arenaviridae viruses), parasitic diseases, bacterial infections, sepsis, cachexia, autolimmune disorders, acute cardiovascular events, chronic myelogenous leukaemia a disorders, acute cardiovascular events, chronic myelogenous leukaemia a
                                                                                                                                                                                                                                                                                                                                                                             transplanted bone marrow-induced graft-versus-host disease, septic immune complex-induced colitis, cerebrospinal fluid inflammation, multiple sclerosis, inflammatory responses associated with trauma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB37791 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel compositions comprising tetracycline or tetracycline-like compounds for the treatment and/or prevention of acute inflammatory responses and diseases, e.g. septic shock and immune complex-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation; infection; sepsis; cachexia; autoimmune disorder; cardiovascular disorder; chronic myelogenous leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-1 receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-FEB-2001
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                                                                                                                                                                                                                                                                                                                             systemic inflammatory response syndrome (SIRS), adult respiratory distress syndrome (ARDS), acute liver failure, inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-2000
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                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                      distress syndrome
and Crohn's diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ANTI-) ANTIBODY SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-APR-2000; 2000WO-US11700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; interleukin-1; IL-1; IL-lalpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antlinflammatory; haemostatic; antibacterial; immunosuppressive;
immunomodulator; cardiant; cytostatic; neuroprotective; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LIGICVAVTVAI 12
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338 migicvtltvii 349
     338
1 LIGICVAVTVAI 12
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38 migicvtltvii 349
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                                                                                                                                                                                                                                                  569
                                                                                                                                                                                                                                                                                                      disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 150-152; 183pp; English
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                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory bowel disease;
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                                                                                                                                         75.0%;
66.7%;
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                                                                                                                                   Score
Pred.
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                                                                                                                  Mismatches
                                                                                                                                      N 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL-1beta;
                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crohn's disease
                                                                                                                                                                Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL-1 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                  bowel disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated
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                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            shock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
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RESULT
AAB30921
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           AAB59700
                         RESULT
                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-1993;
20-DEC-1990;
23-JUL-1996;
                                                                                                                                                                                                                           The present sequence represents a human interleukin-1 (IL-1) polypeptide. The IL-1 polypeptide is used in the method of the invention. The specification describes a method for inhibiting leukocyte infiltration or cartilage degradation in a joint of a mammal. The method comprises administering a viral vector encoding a protein of interest, such that expression of the protein within the joint results in an inhibition of leukocyte infiltration or cartilage degradation in the joint. This protein is an IL-1 receptor antagonist (IRAP), soluble IL-1 receptor, soluble tumour necrosis factor-alpha (TNF-alpha) receptor, IL-10, or their biologically active fragments or derivatives. The method is used for treating connective tissue disorders by inhibiting leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting leukocyte infiltration or cartilage degradation in mammalian joint, comprises administering a viral vector comprising a nucleotide sequence operably linked to a promoter encoding a protein of interest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A human interleukin-1 (IL-1) receptor polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ghivizzani SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; interleukin-1; leukocyte infiltration; cartilage degradation; IL-1 receptor antagonist; IRAP; tumour necrosis factor-alpha receptor;
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AAB59700 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNF-alpha receptor; IL-1.
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                                                                  338
                                                                                                                                                                                                                  infiltration
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migicvtltvii
                                                                                                                     Similarity
8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                             Columns 47-52; 72pp; English.
                                                                                                                                                                                       569
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                 and cartilage degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0027750.
90US-0630981.
96US-0685212.
                                                                                                                                                                                       AA;
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Protein;
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                                                                                                                                  75.0%;
66.7%;
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 569
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                                                                                                                                  Score 42;
Pred. No.
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2; Mismatches
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15;
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                                                                                                                                                22;
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AAB59700;

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RESULT 11
AAY/0708
ID AAY/0707
XX AAY/0707
XX AAY/0707
XX AAY/0707
XX AAY/0707
XX Cancel
XX Cancel
KW Cancel
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XX W09904
XX W09904
XX W09904
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Best Local
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20-OCT-1992;
08-MAR-1993;
18-JAN-1994;
27-JAN-1995;
05-DEC-1995;
23-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; interleuk joint pathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6156304-A
                                                                                                                                                                                                                                                                                                                                The present invention provides a method of producing a protein in the joint of a mammal, involving the intra-articular administration of a viral vector comprising the coding sequence of the desired protein, a where the protein is expressed in a synovial cell. This is useful in treatment of joint pathologies such as arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                             producing a protein in a mammalian joint, for treating mammalian host, by administering a recombinant vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-079537/09.
N-PSDB; AAF24245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glorioso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYPI-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic
                                                                                                                                                                                                                                                                                                                                                                                               Example 3;
                                                                                                                                                                                                                                                                                                                Sequence
                                                                       Cancer associated antigen; diagnosis; breast cancer; colon cancer; gastric (
                                                             prostate cancer.
                                                                                                     Renal cancer
                                                                                                                          02-JUL-1999
                                                                                                                                               AAY07078;
                                                                                                                                                                  AAY07078 standard; Protein;
 28-JAN-1999
                     WO9904265-A2
                                                                                                                                                                                                                   :||||| :|| |
338 migicvtltvii 349
                                                                                                                                                                                                                                         1 LIGICVAVTVAI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-1 receptor; arthritis; retroviral vector;
                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     acid encoding the protein
                                                                                                                                                                                                                                                               Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JC,
                                                                                                                                                                                                                                                                                                                                                                                                 Fig 8; 60pp; English.
                                                                                                                                                                                                                                                                                                                 569 AA;
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                                                                                                                                                                                                                                                               Conservative
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93US-0027750.
94US-0183563.
95US-0381603.
95US-0567710.
96US-0685212.
                                                                                                      associated antigen precursor sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans CH,
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0924777
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                                                                                                                                                                                                                                                                           75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robbins
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                                                                                                                                                                                                                                                                  2:
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Pred. No.
                                                                                                                                                                                                                                                                  red. No. 15;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD;
                                                                           cancer;
                                                                                     research;
                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating arthritis in inant vector comprising a
                                                                                                                                                                                                                                                                                       22;
                                                                            renal
                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                      Length 569;
                                                                             treatment;
nal cancer;
                                                                                                                                                                                                                                                                    Indels
                                                                               lung cancer;
                                                                                          human;
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RESULT 12
AAW43422
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Query Match
Best Local Similarity
Matches 7; Conserv
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17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a a nucleic acid molecule (NAM). The method comprises: (a) contacting a product of a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a interaction between the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and line cancer and cancer and cancer and cancer and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 484; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                      Binding domain; rat; syntaxin; synaptosomal-associated protein; CNS; neurotransmitter; presynaptic membrane; central nervous system; tumou neurodegenerative disease; hormonal disorder; immunological disorder
                                                                                                                                                                                                                                                                  AAW43422 standard;
                                                                                                                                                                              Rat syntaxin 4 protein
                                                                                                                                                                                                                                       AAW43422;
                                                                   US5693476-A.
                                                                                            Rattus
                                                                                                                                                                                                           27-APR-1998
                                                                                                                                                                                                                                                                                                                                     275 liaicvsitvvl 286
           24-FEB-1995;
                                        02-DEC-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer.
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97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
97GB-0021697.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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Sahin
              9508-0393985
                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                           71.4%;
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Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB
Pred. No. 17;
3; Mismatches
                                                                                                                                                                                                                                                                      298 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stockert
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AAB56914
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This amino acid sequence represents the rat syntaxin 4 protein. The invention relates to a method for identifying a compound capable of affecting the binding of a syntaxin-binding period, e.g. SNAP-25, alpha-SNAP, n-secl or VAMP, to syntaxin. The method comprises measuring the effect of the test compound on the extent of binding between the SBP and the SBP-binding site on syntaxin. The method can be used for
                                                                                                                                                                                                                                                                                                      Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening assay for modulators of syntaxin binding - using peptide comprising binding site of syntaxin, for identifying drugs useful for treating CNS disorders, neuro-degenerative diseases, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 51-54; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB56914;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Prostate cancer associated gene sequences, referred to as prostate
                                                                                                                                                                          08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                   WO200055174-A1
                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cancer antigen protein sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying drugs capable of inhibiting or stimulating neurotransmitter release at the active zones of presynaptic membranes, which may be useffor treating CNS disorders, affective or psychotic disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-1995;
                                                                        Rosen CA,
                                                                                                  (HUMA-) HUMAN GENOME SCI INC
(ROSE/) ROSEN C A.
                                                                                                                                              12-MAR-1999;
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hes 8; Conserv
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                            2000-587513/55
DB; AAF16117
                                                                                                                                                                                                                                                                                            infectious disease.
                                                                       Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                              99US-0124270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 380
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66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hormonal or immunological disorders, tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB
Pred. No. 17;
2; Mismatches
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17;
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AAR91951
ID AARS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and prolliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer antigens, useful for treatment, prevention, and diagnosis disorders such as prostate cancer \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                Non-small cell lung carbonic anhydrase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR91951;
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                                                                                                                       01-FEB-1996.
                                                                                                                                                WO9602552-A1
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung cancer specific antigen HCAVIII mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91951 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                      (CYTO-) CYTOCLONAL PHARM INC
                                                                                           19-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 1928-1930; 2338pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinfective, gynaecological and antibacterial activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
                                                                   94US-0276919.
                                                                                             95WO-US09145
                                                                                                                                                                                                                    /label= N-glycosylation_site 895..906
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                               /label= N-glycosylation_site 202
                                                                                                                                                                                         /note= "the phosphorylation site is recognised
                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                      /label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                /label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                cancer; NSCLC; tumour marker; HCAVIII;
diagnosis; therapy; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.4%;
58.3%;
                                                                                                                                                                                                       Phosphorylation_site
                                                                                                                                                                          protein kinase C and other kinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
22;
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Bollon AP,

Torczynski RM;

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RESULT 1
AAR91955
Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 44-46; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding the lung cancer specific antigen HCAVIII useful for diagnosis and treatment of non-small cell lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-105844/11.
N-PSDB; AAT15449.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR91955 standard; Protein; 325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-small cell lung carbonic anhydrase; phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCAVIII phosphorylation-modified (S302G) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91955;
                                                                                                                                                                                                                                                                                                                                                                                                                             WO9602552-A1
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284 ilgicivvvvsi 295
                                                                                                                                                                              Nucleic acid encoding the lung cancer specific antigen HCAVIII useful for diagnosis and treatment of non-small cell lung cancer
                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996
                                          A cDNA sequence (AAT15454) codes for a phosphorylation-modified form (AAR91955) of HCAVIII, a cell surface antigen which is highly specific for non-small cell lung carcinoma (NSCLO) and which has features in common with human carbonic anhydrases. The modified HCAVIII has glycine substituted for serine at position 302 of the mature protein. It is used to study the role of HCAVIII serine
                                                                                                                                                   Claim 16; Page 59-60; 87pp; English.
                                                                                                                                                                                                                                                                                                     (CYTO-) CYTOCLONAL PHARM INC
                                                                                                                                                                                                                                                                                                                                    19-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                 19-JUL-1995;
                                                                                                                                                                                                                               WPI; 1996-105844/11.
N-PSDB; AAT15454.
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                              mature protein. It is used to phosphorylation in oncogenesis.
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      325
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      AA;
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; NSCLC; tumour marker;
diagnosis; therapy; antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCAVIII;
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Query Match
Best Local S
Matches 6
 Similarity
6; Conserv
   Conservative
           69.6%;
     4;
            score 39;
pred. No.
      Mismatches
            DB 17; Length 325; 28;
       2
       Indels
         0;
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Qy В 284 ilgicivvvvsi 1 LIGICVAVTVAI 12 295

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Search con Job time: me: 88 sec November 13, 2001, 14:27:42 THIS PAGE BLANK (USPTO)

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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                       Result
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  2255244
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                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq
  Issued_Patents_AA:*
1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
6: /cgn2_6/ptodata/2
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length: 2000000000
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  BLOSUM62
Gapop 10.0 , Gapext 0.
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Listing first 45 summaries
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56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212252 seqs, 22503292 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGICVAVTVAI 12
                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/backfiles1.pep:*
                                                                                                                                                                                                                                                                              Length
  BB
US-07-821-716-2
US-08-24-376-2
US-08-685-212-2
PCT-US94-02414-2
PCT-US94-08899-2
US-08-376-919-4
US-08-776-088-4
US-08-776-088-4
US-08-776-088-4
PCT-US95-09145A-4
PCT-US95-09145A-4
PCT-US95-09145A-8
PCT-US95-09145A-1
US-08-776-088-6
US-08-776-088-6
US-08-776-088-7
US-08-776-088-7
US-08-776-088-7
US-08-776-088-7
US-08-76-919-2
PCT-US95-09145A-2
PCT-US95-09145A-2
PCT-US95-09145A-3
US-08-659-65-76-1
US-08-659-76-1
US-08-659-76-1
US-08-659-76-1
US-08-659-76-1
US-08-659-76-27
US-08-762-500-27
US-08-569-853-1
US-08-569-853-1
US-08-569-853-1
US-08-569-853-1
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                                                                                                                                                                                                                                                                                                          SUMMARIES
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10.050 Million cell updates/sec
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Sequence
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US-07-821-716-2
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 5 | 34 | 3 3 | 32 | 31 | 30 | 29 | 28 |
|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|
| 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 35 | 35 |
| 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 62.5 | 62.5 |
| 265 | 265 | 249 | 249 | 177 | 173 | 127 | 124 | 51 | 51 | 51 | 15 | 15 | 15 | 15 | 15 | 465 | 462 |
| Ν | N | N | | 4 | 4 | 4 | 4 | 4 | 4 | 4 | ω | N | N | _ | Н | w | ω |
| US-07-857-224B-66 | US-07-857-224B-65 | us-08-690-096-10 | US-07-940-605A-10 | US-08-789-333F-44 | US-08-789-333F-42 | US-08-789-333F-43 | US-08-789-333F-41 | US-09-133-944-14 | US-09-169-015-24 | US-08-789-333F-14 | US-08-466-680B-45 | US-08-468-545B-45 | US-08-486-348A-45 | US-08-414-417B-45 | US-08-467-083-45 | US-08-788-231A-17 | US-08-788-231A-15 |
| Sequence 66, | • | • | ` | ` | • | • | • | • | - | Sequence 14, | - | • | • | • | Sequence 45, | • | • |
| App1 | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl |

ALIGNMENTS

Sequence 2, Application US/07821716 Patent No. 5319071 GENERAL INFORMATION:
APPLICANT: Dower, Steven K
APPLICANT: March, Carl J.
APPLICANT: Sims, John
APPLICANT: Urdal, David L. SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/821,71
FILING DATE: 1920114
CLASSIFICATION ENTA: 1920114
CLASSIFICATION DATA: 1920124
APPLICATION NUMBER: US 125627
FILING DATE: 25-NOV-1987
PRIOR APPLICATION DATA: US 160550
APPLICATION NUMBER: US 160550
APPLICATION NUMBER: US 160550
APPLICATION NUMBER: US 258756
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691551
APPLICATION NUMBER: US 691551
APPLICATION NUMBER: US 691551 TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acids FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2001-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex C NUMBER OF SEQUENCES: 6 COMPUTER: IBM PC OPERATING SYSTEM: Washington E: Immunex Corporation 51 University Street IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1 Floppy disk US/07/821,716 . . . 25

Tue

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MOLECULE TYPE: protein US-07-821-716-2
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US-08-381-603-2
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                     Вр
                                                                                                                                                δÃ
                                                           US-08-924-376-2
                                                                           RESULT
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Matches
Sequence 2, Application US/08924376
Patent No. 6199464
GENERAL INFORMATION:
APPLICANT: Glorioso, Joseph C.
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Robbins, Paul D.
TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue
TITLE OF INVENTION: Mammalian Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEFAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (47)
TELEFAX: 866172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMAN DE PC-TOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street Suite 3232
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LIGICVAVTVAI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/381,603
                                                                                                                        338 MIGICVTLTVII 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                 Local Similarity 66.
                                                                                                                                       1 LIGICVAVTVAI 12 : | | | | | | |
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66.7%;
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Pred. No. 11;
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pred. No. 1
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                                                                                                                                                                                                                                                                                                                           US-08-685-212-2
                                                                                                                                                                                                                                                                                                                                         RESULT
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Best Local
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ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street Suite 3232
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Gene Transfer For Treating a TITLE OF INVENTION: Connective Tissue of a Mammalian Host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEFAX: (215) 575-6015
TELEX: 866172
TELEX: 866172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis |
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/924,376
FILING DATE:
CLASSIFICATION:
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                 ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
                                                                                                                                                                                       APPLICANT: Bandara, Geethani
TITLE OF INVENTION: Gene Transfer For Treating a
TITLE OF INVENTION: Connective Tissue of a Mammalian Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street Suite 3232
CITY: Philadelphia
                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                        NUMBER OF SEQUENCES:
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Gy: linear
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Evans, Christopher H.
Robbins, Paul D.
                                                                                        USA
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08-MAR-1993
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66.7%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 109070-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEPHONE: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                  TELEFAX: (215) 575-6015
TELEX: 866172
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Gene Transfer For TITLE OF INVENTION: a Mammalian Host NUMBER OF SEQUENCES; 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/027,750
APPLICATION NUMBER: US/08/027,750
ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REGISTRATION NUMBER: 25,077
                                SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 109070-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEFAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
   MOLECULE TYPE:
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nes 8; Conserv
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
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                   TOPOLOGY:
                                                                                                                                                                                                                                                           CLASSIFICATION:
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1700 Market Street Suite 3232
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protein
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66.7%;
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Pred. No.
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11;
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Query Match
Best Local Similarity
Watches 8; Conserve
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            Sequence 10, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9608899 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: GOULD, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 109070-12A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: University of Pittsburgh of the Commonwealth APPLICANT: System of Higher Education TITLE OF INVENTION: Gene Transfer For Treating a ConnectTITLE OF INVENTION: Mammalian Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (215) 575-6000
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                      338 MIGICVTLTVII 349
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CTTY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
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1700 Market Street Suite 3232
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66.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                           Score 42;
Pred. No.
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                                                  for Modulation
                                                                                                                                                                                                                                                                                                          Length 569;
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ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

CA

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MOLECULE TYPE: protein US-08-393-985-10
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US-08-276-919-4
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ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPAX: (415) 324-0960
INFORMATION: TOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 4, Application US/08276919
Patent No. 5589579
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Nelligan, Mark C.
REGISTRATION NUMBER: 36,389
REFERENCE/DOCKET NUMBER: B35792
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TOTCZYDSAL,...
APPLICANT: BOILON, Arthur P.
APPLICANT: BOILON: Lung Cancer Marker
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: RICHARDS, MEDLOCK & ANDREWS
ATREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/276,919 FILING DATE:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFRANDED: Details PC-DOS/MS-DOS
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COUNTRY: US
OTD: 75270-2197
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8; Conserva
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MOLECULE TYPE: protein US-08-276-919-4
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                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-276-919-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TOFOCRYSKI, RICHARU ...
APPLICANT: TOFOCRYSKI, RICHARU ...
APPLICANT: BOLLON, Arthur P.
APPLICANT: BOLLON, Lung Cancer Marker
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ANDRESSEE: RICHARDS, MEDLOCK & ANDREWS
ANDRESSEE: RICHARDS, MEDLOCK & ANDREWS
ANDRESSEE: RICHARDS, MEDLOCK & ANDREWS
RESULT 10
US-08-776-088-4
                                                                Дb
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GENERAL INFORMATION:
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                                                                                                                 Query Match
Best Local Similarity
6; Conser
                                                                                                                                                                                                                                                                                  TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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284 ILGICIVVVVSI 295
                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: B3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Nelligan, Mark C.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1201
CITY: Dallas
STATE: TX
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                                                               284 ILGICIVVVVSI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 75270-2197
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                   LENGTH:
                                                                                             1 LIGICVAVTVAI 12
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)GY: linear
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50.0%;
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Pred. No. 19;
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Pred. No.
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19;
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Sequence 4, Application US/08776088 Patent No. 5773579

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GENERAL INFORMATION:

APPLICANT:

Torczynski, Richard M

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Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 18, Application US/08776088 Patent No. 5773579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/776,088
ETLING DATE: 19-JUL-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Eugenia S. Hansen
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 10365/0501
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
TELEFAX: 24-981-3400
TELEFAX: 25-981-3400
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Torczynski, Richard M.
APPLICANT: Bollon, Arthur P.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIDLEY & AUSTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,088
FILING DATE: 19-JUL-95
CLASSIFICATION: 435
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
                 ATTORNEY/AGENT INFORMATION:
NAME: Eugenia S. Hansen
REGISTRATION NUMBER: 31,966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bollon, Arthur P. TITLE OF INVENTION: Lung Car
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CITY: Dallas
STATE: TX
                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 325 amino
TYPE: amino acid
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CITY: Dallas
REFERENCE/DOCKET NUMBER:
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ZIP: 75270-2197
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50.0%;
10365/05011
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Pred. No. 19;
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Query Match
Best Local Similarity
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Best Local Similarity
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RESULT 13
PCT-US95-09145A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIF: /// COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: John A. Harre
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 214-981-3300
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                           MOLECULE TYPE: protein
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284 ILGICIVVVVSI 295
                                                             284 ILGICIVVVVSI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1201
CITY: Dallas
STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
TYPE: a
                                                                                                                                                                                                                          LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 75270-2197
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                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                          1 LIGICVAVTVAI 12
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                                                                                                                        Conservative
                                                                                                                                      69.6%;
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50.0%;
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Pred. No.
                                                                                                                                      Score 39; DB 5;
Pred. No. 19;
                                                                                                                      Mismatches
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                                                                                                                                                    Length 325;
                                                                                                                      Indels
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Sequence 18, Application PC/TUS9509145A GENERAL INFORMATION:

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APPLICANT:
TITLE OF INVENTION: LUI
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

Lung Cancer Marker 22

STREET:

ADDRESSEE:

E: RICHARDS, MEDLOCK & ANDREWS 1201 Elm Street, Suite 4500

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; .MOLECULE TYPE: protein PCT-US95-09145A-18
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: John A. Harre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,919
                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Torczynski, Richa
APPLICANT: Bollon, Arthur P.
TITLE OF INVENTION: Lung Can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 75270-2197
                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 ILGICIVVVVSI 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LIGICVAVTVAI 12
                                                                FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                COUNTRY:
NAME: Nelligan, Mark C. REGISTRATION NUMBER: 36,389 REFERENCE/DOCKET NUMBER: B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acids
                                                                                                                                                                                                                  75270-2197
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Pred. No. 19;
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-276-919-2
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                                                                                                                                               ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-776-088-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity ov...
6; Conservative
 В
                                                    Query Match
Best Local Similarity
Thes 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENGTH: 354 amino acid
                                                                                                                                                                                                                              TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 214-939-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Torczynski, Richard M.
APPLICANT: Bollon, Arthur P.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,088
FILING DATE: 19-UUL-95
FILING DATE: 19-UUL-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: FLOPPY
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Eugenia S. Hansen
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 ILGICIVVVVSI 324
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313 ILGICIVVVVSI 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Dallas
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                               1 LIGICVAVTVAI 12
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50.0%;
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Pred. No.
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                                                                      score 39; DB
Pred. No. 21;
4; Mismatches
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Search completed: November 13, 2001, 14:26:50

Job time: 36 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Query
Match Length DB
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Gapop 10.0 , Gapext 0.5
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56
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pir2:*
pir3:*
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В

7 LIGICVAVTVAI

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| 0у 1 | Query M Best Lo Matches | RESULT 2 T28555 hypothetica. C: Species: \ C: Jate: 22-(C: Jate: 22-(C: Accession R: Massung, I Nature 366, A: Title: Po A: Reference A: Accession A: Status: Pi A: Molecule A: Residues: A: Cross-ref A: Experimen | Query Matches Matches Qy 1 Db 7 | RESULT E36849 Al3L proto C;Species C;Date: 3 C;Accessi R;Blinov, submitted A;Referen A;Accessi A;Molecula A;Residue: A;Cross-rv | | 4444433333333 5443210 |
|-------------------|--|--|---|--|------------|---|
| 1 LIGICVAVTVAI 12 | Query Match 100.0%; Score 56; DB 2; Length 68; Best Local Similarity 100.0%; Pred. No. 0.0083; Matches 12; Conservative 0; Mismatches 0; Indels 0; | protein Al4L - variola major virus virulence_revision 22-Oct-1999 #text_change virulence determinants in terminal regions of number: Z20488; MUID:94088747 virulence determinants in terminal regions of vir | ry Match 100.0%; Score 56; DB 2; Length 68; t Local Similarity 100.0%; Pred. No. 0.0083; ches 12; Conservative 0; Mismatches 0; Indels 0; 1 LIGICVAVTVAI 12 | RESULT 1 B36849 Al3L protein - variola virus (strain India-1967) C;Species: variola virus C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-C;Accession: E36849 R;Blinov, V.M. submitted to GenBank, November 1992 A;Reference number: A36859 A;Reference number: A36859 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-68 <bli>A;Residues: 1-68 <bli>A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49058.1; PID:g29729</bli></bli> | ALIGNMENTS | 36 64.3 364 2 G86340 36 64.3 366 2 T27257 36 64.3 422 2 S52578 36 64.3 457 2 T46332 36 64.3 1472 2 T02458 36 64.3 1472 2 B54774 36 64.3 1529 2 A59189 36 64.3 1529 2 A59189 36 64.3 2233 1 ZLNZP3 35 62.5 134 2 I46090 35 62.5 134 2 I46091 35 62.5 134 2 S56958 35 62.5 157 2 S56958 35 62.5 184 2 B72168 35 62.5 184 2 R36852 35 62.5 184 2 R36852 |
| | Gaps 0; | 21-Jul-2000 .R.; Knight, J.C. variola smallpox | Gaps 0; | ar-2001 | | protein F2D10.35 hypothetical prote serine/threonine-s hypothetical prote for casset genome polyprotein ubiquinolcytochr ubiquinolcytochr hemoglobin alpha c probable olfactory probable membrane A37R protein - var A36R protein - var A36R protein - var |
| | | x vir | | | | |

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A14L protein - variola minor virus (strain Garcia-1966)
A14L protein - variola minor virus
C;Species: variola minor
C;Accession: C72165
C;Accession: C72165
Submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A;Reference number: A72150
A;Reference number: A72150
A;Status: preliminary
A;Status: preliminary
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-68 <SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54717.1; PID:e1542673; PID:g5830678
A;Experimental source: strain Garcia-1966
C;Geneitos:
A;Gene: A14L
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C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Accession: F42518
R;Johnson, G.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Johnson, G.P.
submitted to GenBank, June
A; Reference number: A33172
A; Accession: F42518
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A; Residues: 1-70 <JOH>
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A;Variety: strain Ankara
A;Variety: strain Ankara
A;Variety: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change
C;Accession: T37400
R;Antoine, G;; Scheiflinger, F; Falkner, F.G.; Dorner, F.
A;Description: The complete genomic sequence of the Modified Vac A;Reference number: Z20877
A;Reference number: Z20877
A;Reference number: T37400
A;Accession: T37400
A;Accession: T37400
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A; Residues: 1-70 <ANT>
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A;Experimental source: strain Ankara
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Pred. No. 0.0085;
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A; Residues: 1-569 <CHU>
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A; Accession: C64637
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Best Local
                                                                                                                                                                                                                                                                                                                                                                 amino acid ABC transporter, permease protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                           A;Residues: 1-237 <TOM>
A;Cross-references: GB:AE000603; GB:AE000511;
C;Superfamily: histidine permease protein M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽
                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA.
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Best Local
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NID:g2314075; PIDN:AAD07984.1;

PID:g231

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A;Gene: GDB:ILIR1; ILIRA; D2S1473; ILIR
A;Cross-references: GDB:125254; OMIM:147810
A;Map position: 2q12-2q12
C;Superfamily: interleukin-1 receptor type I
C;Reywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                             R;Chua, A.O.; Gubler, U.
Nucleic Acids Res. 17, 10114, 1989
Nucleic Acids Res. 17, 10114, 1989
A;Title: Sequence of the cDNA for the human
A;Title: Sequence of the cDNA for the human
A;Reference number: S06928; MUID:90098789
A;Accession: S06928
A;Accession: S06928
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-569 <SIM>
A; Cross-references: GB:M20658
                                                                                                                                                                                                                                               A; Status: translation not shown
                      1 LIGICVAVTVAI 12
MIGICUTLTVII 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                      Conservative
                                                                                                                                                                                                           EMBL:X16896; NID:g33800; PIDN:CAA34773.1; PID:g33801
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                                                                     75.0%;
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Pred. No. 0.
                                                                        Score 42;
Pred. No.
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                                                            Mismatches
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0.039;
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                                                                                           2;
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                                                                    0;
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syntaxin - human
C;Specles: Homo sapiens (man)
C;Specles: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Sep-1999
C;Accession: I38517
R;Ll, H:; Hodge, D.R.; Pei, G.K.; Seth, A.
Gene 143, 303-304, 1994
A;Title: Isolation and sequence analysis of the human syntaxin-encoding gene A;Reference number: I38517; MUID:94266173
A;Accession: I38517
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
Syntaxin 4 - rat
(;Species: Rattus norvegicus (Norway rat)
(;Species: Rottus norvegicus (Norway rat)
(;Date: 06:Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
(;Accession: E48213
R;Bennett, M.K.; Garcia-Arraras, J.E.; Elferink, L.A.; Peterson, K.; Fleming Cell 74, 863-873, 1993
A;Title: The syntaxin family of vesicular transport receptors.
A;Reference number: A48213; MUID:93386759
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-297 <JAG>
A;Cross-references: EMBL:X85784; NID:g758104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  syntaxin-4 - human
C;Speckes: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999
C;Accession: $52726
R;Jagadish, M.N.; Fernandez, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-297 <RES>
A; Cross-references: EMBI
C; Superfamily: syntaxin
                                                                                                                                             RESULT
E48213
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C;Superfamily: syntaxin
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Matches 6; Conserv
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Pred. No. 14;
3; Mismatches
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No. 12;
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A;Molecule type: mRNA
A;Residues: 1-298 <BEN>
A;Cross-references: GB:L20821; NID:g349320;
                                                                                                                                                                                                                              A;Title: Sequence and analysis of the 60 kb conjugative, A;Accession: T43080
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                                                                                                                                                                                                                                                                                          C;Accession: T43080
R;Dougherty, B.A.; Hill, C.; Weidman, J.F.;
Mol. Microbiol. 29, 1029-1038, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: Z19191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: syntaxin
                                                                        C; Superfamily:
                                                                                       A;Genome: plasmid pMRC01
A;Note: ORF00008
                                                                                                                                            A; Experimental source: strain
                                                                                                                                              A;Cross-references: EMBL:AE001272; PIDN:AAC55994.1
A;Experimental source: strain DPC3147
                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-114 <DOU>
                                                                                                                                                                                                                                                                                                                                              C;Species: Lactococcus lactis
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position:
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A; Residues: 1-573 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Lactococcus lactis plasmid pMRC01
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nes 8; Conserv
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8; Conserv
                                                                      Staphylococcus aureus transfer
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61.5%;
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Pred. No.
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Pred. No. 44;
Score 38; DB
Pred. No. 14;
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Conservative

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Mismatches

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Gaps

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C;Accession: T32331
R;Rohlfing, T.; Wohldmann, P.; Biewald, T.
R;Rohlfing, T.; Wohldmann, P.; Biewald, T.
Submitted to the EMBL Data Library, September 1997
Submitted to the sequence of C. elegans cosmid C24H12.
A;Reference number: Z21151
A;Accession: T32331
A;Accession: T32331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C24H12.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32331
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T32331
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A;Molecule type: DNA
A;Residues: 1-207 <ROH>
A;Cross-references: EMBL:AF025451; PIDN:AAB71204.1; GSPDB:GN00020; CESP:C24H12.8
A;Experimental source: strain Bristol N2; clone C24H12
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A;Molecule type: DNA
A;Residues: 1-267 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04161.1; GSPDB:GN00
A;Cross-references: GB:AP001508; GB:BA0000004; NID:g10172890; PIDN:BAB04161.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodur A;Reference number: A83650; MUID:20263314
A;Accession: B83705
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A; Introns: 27/3; 53/2; 138/2
probable peptide transport system permease - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: D70729 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; G
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; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID:98295987
A; Accession: D70729
                                                                                                                                                                                                                                                      A;Cross-references: GB:Z77164; GB:AL123456; NID:g3261615; PIDN:CAB01002.1; PID:g32616
A;Experimental source: strain H37Rv
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C;Superfamily: oligopeptide permease protein oppB
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A; Residues: 1-291 <COL>
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Virology 179:517-563(1990).
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01-OCT-2000 (Rel. 40, Last annotation update)
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MEDLINE=90046906; PubMed=2530587;
Sims J.E., Acres R.B., Grubin C.E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vigers G.P., Anderson L.J., Caffes P., Brandhuber B.J., "Crystal structure of the type-I interleukin-l receptor with interleukin-lbeta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sims J.E., Acres R.B.,
March C.J., Dower S.K.;
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Nature 386:194-200(1997).

PUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-IRA). BETA (I AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-IRA). BIN THE AGONIST LEADS TO THE ACTIVATION OF NE-KAPPA B. THE AGONIST LEADS TO THE ACTIVATION OF NE-KAPPA B. THE AGONIST LEADS TO THE ACTIVATION OF NE-KAPPA B. THE AGONIST LEADS TO THE ACTIVATION OF NE-KAPPA B. THE AGONIST LEADS TO THE ACTIVATION OF NE-KAPPA B. THE AGONIST LEADS TO THE ACTIVATION OF NE-KAPPA B. THE AGONIST LEADS TO THE ACTIVATION OF NEW TOTAL THE ACTIVATION OF NEW T
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"Cloning the interleukin 1 red
Proc. Natl. Acad. Sci. U.S.A.
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MEDLINE=97215904; PubMed=9062194;
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MEDLINE=97215903; PubMed=90
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A36187;
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1ITB; 04-FEB-98
1IRA; 17-JUN-98
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     domain;
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POTENTIAL:
CYTOPLASMIC (POTENTIAL)
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IG-LIKE C2-TYPE DOMAIN.
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Query Match Best Local

Similarity

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RESULT A RESULT A STXA_HUMAN ID STXA_H AC 012846 DT 01.NOV DT 15.JUL DT 30.MAY DE WARMAN ID STXAA ON TISSUE RA HISOLE RA HISOLE RA HISOLE RA HISOLE RA FICHAK RT SEQUEL RA FICHAK RT SUBMI RA FICHAK RA FICHAK RA FICHAK SUBMI RA FICHAK SUBMI RA FICHAK SUBMI RA FICHAK RA SUBMI BIOCH RA FICHAK RA SUBMI RA FICHAK RA SUBMI BIOCH RA FICHAK RA SUBMI RA FICHAK RA F
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EMBL; X85784; CAA59769.1; -.
EMBL; AJ000541; CAA04174.1; -.
EMBL; AF026007; AAB88810.1; -.
HSSP; P32851; 1BR0.
MIM; 186591; -.
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Q12846; Q15525;
01-NOV-1997 (Re
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SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-96332494; PubMed-8760387;
MEDLINE-96332494; PubMed-876087;
MEDLINE-96332494; PubMed-876087;
MEDLINE-96332494; PubMed-876087;
MEDLINE-96332494; PubMed-876087;
MEDLINE-96332494; PubMed-876087;
MEDLINE-96332495;
MEDLINE
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Rae J.L., Shepard A.R.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: POTENTIALLY INVOLVED IN DOCKING OF SYNAPTIC NAT PRESYNAPTIC ACTIVE ZONES.
-I- SIMILARITY: BELONGS TO THE SYNTAXIN/EPIMORPHIN FAMILY.
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STX4A OR STX4,
Homo sapiens (Human).
Horota; Metazoa; Chordata;
Horia; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Peripheral blood Nabokina S., Lazo P.A., submitted (JUL-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Insulin-responsive tissues contain the core (synaptosomal-associated protein 25) A and B syntaxin 4 and synaptobrevins 1 and 2."; Biochem. J. 317:945-954(1996).
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MEDLINE-94266173; PubMed-8206394;
Li H., Hodge D.R., Pei G.K., Seth
"Isolation and sequence analysis"
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STX4A OR STX4.
                                                                                                               Pfam; PF00804; Syntaxin; PROSITE; PS00914; SYNTAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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15-JUL-1998 (Rel. 36, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                    Neurotransmitter
DOMAIN 43
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HSSP;
                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no rest use by non-profit institutions as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               "Characterization of Munc-18c and syntaxin-4 in Putative role in insulin-dependent movement of G. J. Biol. Chem. 272:6179-6186(1997).

-I- FUNCTION: POTENTIALLY INVOLVED IN DOCKING OF AT PRESYMAPTIC ACTIVE ZONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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DOMAIN
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=97197781; PubMed=9045631;
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P70452;
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                                                                                                                                                                                               Pfam; PF00804; Syntaxin;
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8; Conserv
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2; Mismatches
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COILED COIL (POTENT)
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Q1-NOV-1997 (Re
30-MAY-2000 (Re
SYNTAXIN 4.
STX4A OR STX4.
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MEDLINE-93386759; PubMed-7690687;

Mennett M.K., Garcia-Arraras J.E., Elferink L.A., Pettenning A.M., Hazuka C.D., Scheller R.H.;

"The syntaxin family of vesicular transport receptors cell 74.863-873(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; NCBI_TaxID=10116;
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Eukaryota; Metazoa;
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SEQUENCE
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modified and this statement
entities requires a license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- TISSUE SPECIFICITY: HEART, SPLEEN, SKELETAL MUSCLE, At
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L20821; AAA03046.1; HSSP; P32851; 1BR0.
                                                                                                                                                                                                                                                                               CAHC_HUMAN STANDARD; PKT; 3
6/43570; 043570; 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
15-JUL-1999 (Rel. 38, Last annotation
16-JUL-1999 (Rel. 38, Last annotation
16-JUL-1999 (Rel. 38, Last annotation
18-JUL-1999 (Rel. 38, Last annotation
18-JUL-1999 (Rel. 38, Last annotation)
18-JUL-1999 (Rel. 38, Last sequence up
18-JUL-1999 (Rel. 38, Las
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                   SEQUENCE FROM N.A.

MEDLINE=98301622; PubMed=9636197;

MEDLINE=98301622; PubMed=9636197;

Tureci O., Sahin U., Vollmar E., Siemer S., Gottert E.

Tureci O., Sahin G.N., Grubb J.H., Pfreundschuh M.,

Parkkila A.K., Shah G.N., Grubb J.H., pfreundschuh M.,

Parkkila A.K., Shah G.N., Grubb J.H., pfreundschuh M.,

"Human carbonic anhydrase XII: cDNA cloning, expressio

"Human carbonic anhydrase XII: cDNA cloning, expressio

"Human carbonic anhydrase gene

"Chromosomal localization of a carbonic anhydrase gene

"Chromosomal localization of a carbonic anhydrase gene
                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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275 MIAICVSVTVLI
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PS00914; SYNTAXIN;
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pa; Chordata;
la; Rodentia;
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Primates;
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Sciurognathi; Muridae; Murinae; Rattus
              cell cancers
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HOM-RCC-3.1.3).
                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                     dschuh M., Sly W.S.; expression, and
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The carcinoma cell lines by wild-type von Hippel-Lindau transge carcinoma cell lines by wild-type colon, kidney, citational carcinoma cell lines by wild-type carcinoma carcinom
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2_MYCTU
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MIM; 603263;
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Q10623; Q50698;
Q1-CCT-1996 (Rel. 34, Created)
Q1-NOY-1997 (Rel. 35, Last sequence update)
Q1-MAY-2000 (Rel. 39, Last annotation update)
PUTATIVE DEPTIDE TRANSPORT PERMEASE PROTEIN R
RV1282C OR MTCY373.01C OR MTCY3H3.01.
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     STRAIN=H37RV;
MEDLINE=98295987;
Cole S.T., Brosch
                                                                                                                                       Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                          Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Corynebacterineae; My
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PS00162; E
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EUK_CO2_ANHYDRASE;
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R., Parkhill J.,
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Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).

--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
DECTEDIATE APERGRAPH TAYEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
DECTEDIATED TRANSPORT TO STORY OF THE BINDING-
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                                                                                                                                "Molecular analysis of the anaerobic succinate degradation pathway Clostridium kluyveri";
J. Bacteriol. 178:871-880(1996).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-i- SIMILARITY: BELONGS TO THE UPF0077 (PECM) FAMILY.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium kluyveri.
Bacteria; Firmicutes;
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L 33.5 KDA PROTEIN IN CAT1 5'REGION (ORFY).
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                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                  "Gene content and organization of a the extremely thermophilic archaeon, Genome 43:116-136(2000).

i- FUNCTION: INVOLVED IN PROTEIN FXI
                                                                                                                                                                                                                                                                                                                                                                                                            Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C., Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D., Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She O., St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F., St Jean A., Sensen C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-DSM 1617 / P2;
MEDLINE-20165948; pubmed-10701121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed
                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sulfolobus solfataricus. Archaea; Crenarchaeota; Sulfolobales; Sulfolobus
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                                       EMBL; Y18930; CAB57608.1;
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                                                                                                                                                                                                                                             FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE PLEY FORMING PART OF A CHANNEL.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
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                                                                                an email to license@isb-sib.ch).
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Kleinschmidt T., Marz J., Braunitzer G.;
The primary structure of pale-throated three-toed
tridactylus, Xenarthra) hemoglobin.";
Biol. Chem. Hoppe-Seyler 370:303-308(1989).
Biol. Chem. Hoppe-Seyler 370:303-308(1989).
FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE
VARIOUS PERIPHERAL TISSUES.
VARIOUS PERIPHERAL TISSUES.
I- SUBUNIT: TETRAMER OF TWO ALPHA CHAINS AND TWO E

-I- SUBUNIT: TETRAMER OF TWO ALPHA CHAINS AND TWO E

-I- SIBULARITY: BELONGS TO THE GLOBIN FAMILY.
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O1-JAN-1990 (Rel. 13, La
O1-OCT-2000 (Rel. 40, La
HEMOGLOBIN ALPHA CHAIN.
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Edentata; Bradypodidae; Bradypus.
NCBI_TaxID=9354;
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InterPro; IPR002338; -.
Pfam; PF00042; globin; 1.
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                                                                                         Score 37; DB pred. No. 14; 3; Mismatches
                                                                                                                                                                                           iratory protein; Erythrocyte.
IRON (HEME DISTAL LIGAND).
IRON (HEME PROXIMAL LIGAND).; 2808540F975F9435 CRC64;
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                                                                                                          37; DB
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RESULT

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RC MEDLINE-98295987; PubMed=9634230;

RA MEDLINE-98295987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Squres R.,

RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,

RA Ratter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,

RA Ratter S., Seeger K., Skelton S., Squares S., Sqares R.,

RA Cole S., Whitehead S., Barrell B.G.;

Taylor K., Whitehead S., Barrell B.G.;

Taylor K., Whitehead S., Barrell B.G.;

Taylor K., Whitehead S., Barrell B.G.;

The complete genome sequence.";

RI Complete genome sequence.";

RI Complete genome sequence.";

RI Nature 393:537-544(1998).

SI Nature 393:537-544(1998).

BIOSYMTHESIS OF THE CELL WALL PEPTIDOGLYCAN (BY SIMILARITY).

BIOSYMTHESIS OF THE CELL WALL PEPTIDOGLYCAN (BY SIMILARITY).

BIOSYMTHESIS OF THE CELL WALL PEPTIDOGLYCAN (BY SIMILARITY).

C. LYSYL-D-ALANYL-D-ALANYL-D-GLUTAMYL-L-LYSYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANY
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                                                                                                                                                                                                                                                                                                                                                Pfam; pF00953; Glycos_transf_4; pROSITE; PS01347; MRAY_1; 1. pROSITE; PS01348; MRAY_2; 1.
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InterPro; IPR000715; -
Pfam; Pr00953; Glycos_
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or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 4. MRAY
1 LIGICVAVTVAI
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                                                                                                                                                                                                                                                                               SEQUENCE ..... STRAIN-KI2 / MG1655;
MEDLINE-93315143; PubMed-7686882;
MEDLINE-93315143; PubMedt G. III, Da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sarsero J.P., Wookey P.J., Gollnick P., Yanofsky C., "A new family of integral membrane proteins involved aromatic amino acids in Escherichia coll."; J. Bacteriol. 173:3231-3234(1991).
                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                           Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.; "DNA sequence and analysis of 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication."; Genomics 16:551-561(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOW AFFINITY
TNAB OR TRPP
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01-NOV-1997
                                                                                     Transport;
                                                                                              PRINTS; PR00166; AROAAPRMEASE.
PROSITE; PS00594; AROMATIC_AA_PERMEASE_1; 1.
                                                                                                                  InterPro;
                                                                                                                             EcoGene; EG11006; tnaB.
                                                                                                                                        PIR; A39412; A39412.
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                                                                                                                                                 K00032; AAA24677.1; -. M59914; AAA62792.1; -. L10328; AAA62060.1; -. AE000448; AAC76732.1; -.
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                                                                                     Amino-acid
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(TRYPTOPHAN PERMEASE.
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35, Last annotation
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                                                                                     Inner membrane
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Q34462;
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15-JUL-1999 (Rel. 38, Last
30-MAY-2000 (Rel. 39, Last
CYTOCHROME B (FRAGMENT).
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P18974; 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence up
01-JUN-1994 (Rel. 29, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89207099; PubMed=3242545;

Rueckhagel K.P., Braunitzer G., Wiesner H.;

"Hemoglobins of reptiles. The primary structures of the alpha

beta I-chains of common iguana (Iguana iguana) hemoglobin.";

Biol. Chem. Hoppe-Seyler 369:1143-1150(1988).
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  STRAIN-LSUMZ
Sudman P.D.,
                                                                                                        Eukaryota;
Mammalia;
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HSSP; P01922; 1FDH.
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NCBI_TaxID=8517;
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                                         SEQUENCE FROM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEMOGLOBIN ALPHA-1 CHAIN
                                                                                  NCBI_TaxID=27619;
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    PF00042; globin; 1.
TE; PS01033; GLOBIN;
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Eutheria;
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27212; TISSUE-Liver, and Barkley L.J., Hafner M.S
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58 58 IRON (F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iratory protein; Erythrocyte.
IRON (HEME DISTAL LIGAND).
IRON (HEME PROXIMAL LIGAND).
; 9B56DCCCE5DCBF97 CRC64;
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D -> V (IN REF. 3);
; 1E34C7DE3DF6E9D9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 141;
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Search completed: November 13, 2001, 14:34:25 Job time: 396 sec
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                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Familial affinity of Tomopeas ravus (Chiroptera) based on protein electrophoretic and cytochrome b sequence data.";

J. Mammal. 75:365-377(1994).

-i. FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX II OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS.

COUPLED TO ATP SYNTHESIS.

-i. COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY POCKED TO THE GROUPS (B562 AND B566)
                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Busis Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
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METAL
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                                                                                          1 LIGICVAVTV 10
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176 AA;
                                                                                                                                       Conservative
                                                                                                                                                                                                     176
19583 MW; 6C948ACA8905FlA9 CRC64;
                                                                                                                                                                                                                                             83
97
                                                                                                                                                     64.3%;
                                                                                                                                       score 36; DB 1; Length 176;
pred. No. 25;
3; Mismatches 1; Indels
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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4: sp_human:*
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6: sp_mammal:*
7: sp_mhc:*
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10: sp_plant:*
11: sp_rodent:
12: sp_vertebr
13: sp_vertebr
14: sp_virus:*
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Gapop 10.0 , Gapext 0.5
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56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_vertebrate:*
sp_virus:*
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sp_bacteria:*
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09F445
 Q9W4U8
Q9T6R5
Q87996
Q9SJ74
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057225 vaccinia vi
09jf84 vaccinia vi
09jf84 variola vir
089163 variola vir
025593 helicobacte
09p895 neurospora
017654 caenorhabdi
09e207 cercopithec
087210 lactococcus
017160 caenorhabdi
09kfn7 bacillus ha
062368 caenorhabdi
09kfn7 bacillus ha
062368 caenorhabdi
09kfn7 bacillus ha
062368 caenorhabdi
0914d5 pseudomonas
0914d7 klebslella
045385 bordetella
045385 bordetella
031603 bacillus su
09w4u8 drosophila
09t6r5 rana dybows
087996 alcaligenes
                                                                                                                                                                                                      Description
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057225
ID 05
AC 05
DT 01
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
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| 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 |
| 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 64.3 | 66.1 | 66.1 | 66.1 | 66.1 | | | | | | | 66.1 |
| 453 | 453 | 440 | 422 | 380 | 379 | 366 | 364 | 350 | 296 | 266 | 231 | 196 | 134 | 111 | 2233 | 2233 | 2233 | 973 | 966 | 966 | 944 | 599 | 552 | 510 | 502 |
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| 090ZI8 | Q9NRX5 | 075655 | Q40543 | Q9ZZC9 | Q9GAN1 | Q9XWT7 | Q9LM68 | Q31062 | Q9ХЕЛЗ | Q917L7 | Q9TXJ7 | Q9Z663 | Q9XMC9 | 025112 | Q9J7D0 | Q9J7D6 | Q81890 | Q9Y7Q7 | 008794 | Q9P0X0 | Q14697 | P71787 | P91765 | Q9SP15 | Q9SP14 |
| Q9qzi8 mus musculu | Q9nrx5 homo sapien | 075655 homo sapien | Q40543 nicotiana t | Q9zzc9 upupa epops | Q9ganl carollia pe | Q9xwt7 caenorhabdi | Q91m68 arabidopsis | Q31062 sus scrofa | Q9xej3 zea mays (m | Q9i717 drosophila | Q9txj7 caenorhabdi | Q9z663 zymomonas m | Q9xmc9 mormoops me | helicoba | | | Q81890 human parai | Q9y7q7 schizosacch | 4 mus | Q9p0x0 homo sapien | Q14697 homo sapien | P71787 mycobacteri | P91765 myzus persi | Q9sp15 asarina bar | Q9spl4 alonsoa mer |

ALIGNMENTS

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ID 03
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SEQUENCE FROM N.A.

STRAIN=TIAN TAN;

Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang A.A.,

Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;

"Complete genomic sequence of vaccinia virus (Tian Tan strain).";

Submitted (SEP-1988) to the EMBL/GenBank/DDBJ databases.

EMBL; AF095689; AAF34007.1; -.

EMBL; AF095689; AAF34007.1; -.

EMBL; AF095689; AAF34007.1; -.

EMBL; AF095689; AAF34007.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F., Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Pars Esposito J.J., Sosnovtsev S.; "Analysis of the complete coding sequence of DNA of alastrim minor virus strain Garcia-1966.", Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; X76268; CAA53886.1; -. EMBL; Y16780; CAB54717.1; -. SEQUENCE 68 AA; 7569 MW; 32BB8780100737157
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01-MAY-2000
ORF4L.
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=Variola virus; STRAIN=GARCIA-1966; Shchelkunov S.N., Totmenin A.V., Sosnovtsev S.V., Resenchuk S.M., Blinov V.M., Sandakhchiev L.S.; Submitted (NOV-1993) to the EMBL/GenBank/DDBJ data
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Q89163;
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01-JAN-1998
01-JAN-1998
01-JUN-2000
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01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2000 (TrEMBLrel. 14,
AMINO ACID ABC TRANSPORTER,
                                                                                                                                                                                                                                   025593
   Helicobacter
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   pylori (Campylobacter pylori)
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RNA stage; Poxviridae;
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Pred. No.
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Pred. No.
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.069;
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MEDLINE-97394467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.D., Dougherty B.A
Teleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
McKenney K., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                    Q9P8G5
Q9P8G5;
01-OCT-2000
01-OCT-2000
01-MAR-2001
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Nature 388:539-547(1997).
Nature aE000603; AAD07984.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00528; BPD_transp; 1.
Hypothetical protein.
SEQUENCE 237 AA; 26351 MW;
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NCBI_TaxID=210;
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                                                                                                                                                                                    InterPro;
Pfam; PF0(
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                                                                                                                                                                                                                      Gupta G.D., Heath B.I.;
"Neurospora crassa putative
submitted (MAY-2000) to the
EMBL; AF262964; AAF72704.1;
                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota;
Sordariales; Sordariaceae; Neu
                                                                                                                                                                                                                                                                                                                                                       PUTATIVE
                                                                                                                                                                         SEQUENCE
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6; Conserv
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IPR000727;
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AA; 52175 MW;
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16,
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databases.
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PRELIMINARY;

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3 (TrEMBLrel.
3 (TrEMBLrel.
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13,05,

Created)
Last sequence update)
Last annotation update)

C41G6.2 C41G6.2 PROTEIN

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RESULT QUEZOLT OF THE PROPERTY OF THE PROPERTY
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Matches
                                                                                                                                           01-MAR-2001 (TIEMBLIEL 16, Created)
01-MAR-2001 (TIEMBLIEL 16, Last seq
01-MAR-2001 (TIEMBLIEL 16, Last anno
MEMBRANE PROTEIN.
Cercopithecine herpesvirus 7.
VIruses; dsDNA viruses, no RNA stage
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281047; CAB602826.1; -.
EMBL; 283116; CAB60294.1; -
EMBL; 281047; CAB60294.1; JOIN
SEQUENCE 573 AA; 66076 MW;
                                                                                                                                                                                                                                                                 Q9E207;
Q9E207;
Q1-MAR-2001
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Couls
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hiller L., Jier M., Johnston
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan
Parsons J., Percy C., Rifken L., Ropora A., Saunders D., Shownk
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C41Gb.2.
Caenorhabditis elegans.
Cukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; meloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watson A., Weinstock L., Wilkinson-Sproat "2.2 Mb of contiguous nucleotide sequence elegans.";
Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam "Complete Sequence of the Simian Varicella Virus Genome."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cummings P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-99069613; PubMed-9851916;
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                                                                          SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=35245;
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[3]
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76 MIGICIADLTIAI 88
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                                                                                                                                                                  RNA stage;
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017160; TEMB
01-JAN-1998 (TEMB
01-JAN-1998 (TEMB
01-MAR-2001 (TEMB
C24H12.8 PROTEIN.
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01-NOV-1998
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087210;
        Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson .
Craxton M., Dear S., Du Z., Durbin R., Favello, A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
                                                                                                                                                                                                                                                                                                                                                                        "Sequence and analysis of the 60 kb plasmid pMRC01 from Lactococcus lact Mol. Microbiol 29:1029-1038(1998).
EMBL; AE001272; AAC55994.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF275348; AAG27247.1; SEQUENCE 87 AA; 9693 MW;
                                                                    STRAIN-BRISTOL N2; MEDLINE-94150718; PubMed-7906398;
                                                                                                                    Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99000510; PubMed=9767571;
Dougherty B.A., Hill C., Weidman
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                                                                                        SEQUENCE FROM N.A.
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les 6; Conser
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Gremblrel.

Gremblrel.
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  Rifken L.,
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Caenorhabditis.
                                                                                                                                                                                                                                                                                                   Score 38; DB; Pred. No. 26; 4; Mismatches
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Last sequence update)
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Roopra
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is DPC3147.";
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  Α.,
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Best Local S
Matches 5
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STRAIN-BRISTOL N2;
Rohlfing T., Wohldmann P
Submitted (OCT-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of "2.2 Mb of contiguous nucleotide sequence from chromosome III of elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takak
Takami ted (MAR-2000) to the E
EMBL; AP001508; BAB04161.1;
InterPro, IPR000515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9KEN7;
Q9KN7;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotat:
Q1-MAR-2001 (TREMBLREL SYSTEM (PERMEASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368:32-38(1994).
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Submitted (SE
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STRAIN-BRISTOL N2;
062368;
01-AUG-1998 (TrEMBLrel. 0
01-AUG-1998 (TrEMBLrel. 0
01-JAN-1999 (TrEMBLrel. 0
T06G6.2 PROTEIN.
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24415 MW;
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the EMBL/GenBank/DDBJ databases
                         07, Created)
07, Last sequence update)
09, Last annotation update)
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e EMBL/GenBank/DDBJ
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RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Couper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gradner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Nieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT elegans.",
RT elegans.",
RT EMBL; Z81587; CAB04702.1; -.
RE EMBL; Z81587; CAB04702.1; -.
SO SEQUENCE 353 AA; 40782 MW; FA75598667415E45 CRC64;
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Q914D5
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                                                                  RX MEDLINE-2043737; PubMed-10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Bridy L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Bridy L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Bridy L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
R "Opportunistic pathogen.";
R Mature 406:959-964 (2000).
R EMBL; AE004550. AAG04592.1; -.
R Mypothetical protein.
R TAGONASSON AG04592.1; -.
SQ SEQUENCE 135 AA; 14681 MW; 64DBF1D9549A4818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       (Q914D5
Q914D5;
Q91AP5;
Q91AP5;
Q91AP5;
Q1-MAR-2001 (TrEMBLrel. 16, Cr
Q1-MAR-2001 (TrEMBLrel. 16, La
T Q1-MAR-2001 (TrEMBLrel. 16, La
T Q1-MAR-2001 (TrEMBLrel. 16, La
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       Pseudomonas
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54.5%;
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Pred.
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Best Local
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01-NOV-1998 (
01-NOV-1998 (
PUTATIVE GTG
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- CAPALYTIC ACTIVITY: CLEAVAGE OF N-TERMINAL LEADER SEQUENCES FROM MEMBRANE PROLIPOPROTEINS. HYDROLYSES XAA-XBB-XBB-|-CYS, IN WHICH XAA IS HYDROPHOBIC (PREFERABLY LEU), XBB IS OFTEN SER OR ALA, XCC IS OFTEN GLY OR ALA, AND THE CYS IS ALKYLATED ON SULFUR WITH A DIACYLGLYCERYL GROUP (BY SIMILARITY).

- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

- IS SIMILARITY: BELONGS TO PEPTIDASE FAMILY AB.

EMBL; AF201388; AAF19640.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Independent Expression and Iron Regulation of the lsp (
*Independent Expression and Iron Regulation of the lsp (
*Klebsiella pneumoniae.",
*Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: THIS PROTEIN SPECIFICALLY CATALYZES THE RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-MAR-2001 (TrEMBLrel. 16, L
LIPOPROTEIN SIGNAL PEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01252; Peptidase_A8; 1.
PRINTS; PR00781; LIPOSIGFPASE.
PROSITE; PS00855; SPASE_II; 1.
Aspartyl protease; Hydrolase; Lipoprotein; Transmembrane.
SEQUENCE 166 AA; 18410 MW; 474857EDCDDC85EF CRC64;
MEDLINE=96419162; PubMed=8821935;
Allen A.G., Maskell D.J.;
"The identification, cloning and required for lipopolysaccharide b
                                                                                                                                                                                                                             Bordetella pertussis.
Bacteria: Proteobacteria:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF201388; AAF19640.1; -.
InterPro; IPR001872; -.
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Klebsiella
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                                                                                                     STRAIN-BP536
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                          Bordetella
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7; Conserv
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d mutagenesis
biosynthesis
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3.4.23.36) (PROLIPOPROTEIN SIGNAL
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Bordetella
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RA AZEVEGO V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA BOURISER E., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA BOURISER E., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Galleron N.,
RA Choi S.K., Codani J.J., Haga K., Haiech J., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gulseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Meilado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parecon E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Raivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Sekiguchi A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Vassarotti A.,
RA Takeuchi M., Weller E., Wedler E., Weller E., Weller H., Weitzenegger T.,
RA Winter S., Caname S., Vandonbol M., Vannier F., Vassarotti A.,
RA Voshida K., Yoshikawa H
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O31603;
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Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
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Mol. Microbiol. 19:37-52(1996).
EMBL; X90711; CAA62254.1; -.
SEQUENCE 193 AA; 21015 MW;
STRAIN=168;
Kunst F., Ogasawara N., Yoshikawa H., Danchin Submitted (NOV-1997) to the EMBL/GenBank/DDBJ EMBL; 299110; CABL3008.1; -.
SEQUENCE 218 AA; 23745 MW; EA254C8E95A9070
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01-NOV-1998
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                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.1%;
75.0%;
                                                                                                                                                                                                                                                                             , Yamamoto H., Yamane K., Yasumoto K., a H.F., Zumstein E., Yoshikawa H., Dan sequence of the gram-positive bacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05,
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         EA254C8E95A90700 CRC64;
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                       and is
                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                    re greater than or equal to the score of the result being is derived by analysis of the total score distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq
       A_Geneseq_0601:*

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2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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AAP50222
AAP50222
AAP60127
AAP601403
AAP60576
AAP70922
AAP90630
AAR15713
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AAR26689
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                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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13.377 Million cell updates/sec
Luteinising Hormon Luteinising Hormon Conadotrophin relea Gonadotrophin relea Novel decapeptide Luteinising hormon Sequence of lutein Peptide #1 with ho LH releasing hormon LHRH hapten for at
                                                                                                                                                                                                                                                                         Description
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 8 | 37 | 36 | 35 | 34 | ω ω | 32 | <u>ယ</u> ည | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|-------------------|----------|--------------------|----------|--------------------|----------|-------------|-------------------|
| 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 | 63 |
| 100.0 | | | • | 100.0 | 00. | | | • | • | 100.0 | 100.0 | 100.0 | | 100.0 | 100.0 | • | 100.0 | • | | • | | 100.0 | | • | | • | | | • | 100.0 | 100.0 | 0 | 100.0 |
| 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| 22 | 22 | 22 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20. | 19 | 18 | 18 | 17 | 17 | 16 | 16 | 16 |
| AAB68693 | AAB73047 | AAB71947 | AAY55061 | AAY58136 | AAY68566 | AAY91197 | AAY79054 | AAY82376 | AAY88576 | AAB06261 | AAB03590 | AAB08103 | AAY96084 | AAB20777 | AAB20863 | AAB15362 | AAB10930 | AAW83360 | AAW84278 | AAW96765 | AAW94890 | AAY03856 | AAY31067 | AAY31176 | AAY50229 | AAW76373 | AAW04612 | AAW45642 | AAW65203 | AAW65201 | AAR75152 | AAR86845 | AAR91197 |
| Luteinising Hormon | Mammalian luteinis | GnRH monomer pepti | Luteinising hormon | Native mammalian g | Luteinising hormon | | Luteinising hormon | Mammalian releasin | Gonadotrophin-Rele | Gonadotrophin rele | Luteinising hormon | Amino acid sequenc | Gonadotropin relea | Luteinising hormon | Gonadotropin relea | Human LHRH peptide | Gonadorelin peptid | Luteinising hormon | Hormone domain of | Luteinising hormon | LHRH peptide fragm | Amino acid sequenc | inked p | Ubiquitin fusion p | Neutrophil-activat | Rat GnHR peptide. | 7 | Luteinising hormon | | Luteinising hormon | | dotropin re | ьнкн peptide. Syn |

ALIGNMENTS

RESULT AAP10411 ID AAP1

AAP10411 standard;

peptide;

10

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17-DEC-1992

(first entry)

AAP10411;

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Key
Modified-site
                                                                                                                                                                                              dysmennorhea; precocious puberty; endometriosis; prostate cancer; benign prostate hypertrophy; mammary tumour.
LH-RH, liberating factor for LH and
                   WPI; 1981-23409D/14 (23409D).
                                                                                                                                                                                                                 LHRH; Follicle Stimulating Factor; FSH; acne; hirsutism;
                                                                                                                                                                                                                                   Luteinising Hormone Releasing Hormone.
                                                        21-SEP-1979;
                                                                          23-FEB-1983;
                                                                                                             BE885308-A.
                                                                                                                                         Modified-site
                                     (ROUS ) ROUSSEL UCLAF.
                                                                                           19-MAR-1981
                                                       79FR-0023545
                                                                          83BE-0468932.
                                                                                                                                        /note=
                                                                                                                                                                             Location/Qualifiers
                                                                                                                               /note= "amidated"
                                                                                                                                                           /label- OTHER
                                                                                                                                                 "pyroglutamic
FSH,
                                                                                                                                                  acid"
and its agonists compsn.
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RESULT
AAP10416
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A composition is claimed containing LHRH or its analogues. The composition is used to treat prostate adenocarcinoma, benign hypertrophy of the prostate, endometriosis, dysmenorrhea, hirsutism hormone-dependent mammary tumours, for treatment or prevention of precocious puberty, delaying the onset of puberty and for treating acne. The compositions may also contain antiandrogens. see also AAP10412-P10418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - used to treat prostate adenocarcinoma, benign hypertrophy the prostate, hirsutism, acne, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1(a); Page 15; 27pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP10416 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                  LHRH; Follicle Stimulating Factor; FSH; acne; hirsutism; dysmennorhea; precocious puberty; endometriosis; prostate cancer; benign prostate hypertrophy; mammary tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Luteinising Hormone Releasing Hormone analogue #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-DEC-1992
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                                                                                                                                                                                                                                                                                                              Modified-site
A composition is claimed containing LHRH or its analogues. The composition is used to treat prostate adenocarcinoma, benign hypertrophy of the prostate, endometriosis, dysmenorrhea, hirsutism hormone-dependent mammary tumours, for treatment or prevention of precocious puberty, delaying the onset of puberty and for treating
                                                                                          LH-RH, liberating factor for LH and FSH, used to treat prostate adenocarcinoma, the prostate, hirsutism, acne, etc.
                                                                                                                                            WPI;
                                                                                                                                                                                                                                         19-MAR-1981
                                                                     Claim 1(f); Page 16; 27pp; French.
                                                                                                                                                                                         21-SEP-1979;
                                                                                                                                                                                                                   23-FEB-1983;
                                                                                                                                                                   (ROUS ) ROUSSEL UCLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EHWSYGLRPG 10
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                                                                                                                                              1981-23409D/14 (23409D).
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                                                                                                                                                                                             79FR-0023545
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                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                       'label= OTHER
                                                                                                                                                                                                                                                                                                                                                                          'label=
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                                                                                                                                                                                                                                                                                                                                                            "pyroglutamic acid"
                                                                                                                                                                                                                                                                                                                            "N-alpha-methyl-Leu'
                                                                                                                                                                                                                                                                                                                                                                           OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63; DB 2; Fred. No. 0.00012; Pred. No. 0.00012;
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                                                                                                              and its agonists compsn-
benign hypertrophy of
                                                                                                                                                                                                                                                                                                          in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                  hirsutism,
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See A
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                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-1983;
30-AUG-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP50222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gonadotrophin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1985
                                                                                                                                                                                                  The claimed peptide antagonists inhibit the release of gonadotrophins and/or steroids. They are antagonistic to GnRH, inhibit ovulation, and may cause resorption of a fertilised egg if administered shortly after absorption. The peptides also have utility in male contraception, and in treatment of precoscious puberty, hormone dependent neoplasia, dysmenorrhoea and endometriosis.
                                                                                                                                                                                                                                                                                                      New GnRH antagonist peptide(s) - useful as inhibitors of gonadotropin(s) and/or steroid(s) for contraceptive use.
                                                                                                                                                                                                                                                                                Disclosure; Page 1; 20pp; English.
                                                                                                                                                                                                                                                                                                                                       WPI; 1985-136434/23
                                                                                                                                                                                                                                                                                                                                                            Roeske
                                                                                                                                                                                                                                                                                                                                                                                  (SALK ) SALK INST FOR BIOL STUD
                                                                                                                                                                              Sequence
                      AAP60127 standard; Peptide;
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 {\tt AAP10411-P10418}\,.
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1 ehwsyglrpg
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|ehwsyglrpg 10
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10; Conserv
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                                                                                                                                                                                 10 AA;
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         release stimulating hormone
                                                                                                                                                                                                                                                                                                                                                                                                          83US-0556148.
85US-0771517.
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100.0%;
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Pred.
                                                                                                                             0;
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                                                                                                                            Score 63; DB 6;
pred. No. 0.00012;
); Mismatches 0;
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0.00012;
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AAP60127;

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RESULT
AAP61403
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Best Local S
Matches 10
Prepn. of gonadotropin liberating hormone and analogues - by multistage rapid peptide synthesis in soln. without isolating
                                                                                                                                                         Gonadotropin releasing hormone; ovulation; veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide gonadotropin releasing hormone antagonists - esp. as contraceptives, for treating early puberty, hormone-dependent neoplasms etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rivier JEF, Varga JI,
Rivier CL, Vale WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP201260-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conadoliberin
                                                                                  08-MAY-1984;
                                                                                                    08-MAY-1984;
                                                                                                                                         DD232500-A
                                                                                                                                                                                    Gonadotropin releasing hormone.
                                                                                                                                                                                                      04-AUG-1991
                                                                                                                                                                                                                          AAP61403
                                                                                                                                                                                                                                           AAP61403 standard;
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   The decapeptide encodes a gonadoliberin antagonist, which may be used as a male contraceptive and as an antitumour (against steroid-
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 1; 33pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1986-299774/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gonadoliberin antagonist; contraceptive; antitumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-1991
                           WPI; 1986-137868/22
                                                               (DEAK ) AKAD
                                                                                                                      29-JAN-1986
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                                                                                                                                                                                                                                                                                                                                                                                          tumours).
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                                                                                                                                                                                                      (first entry)
                                                               WISSENSCHAFT DDR.
                                              Dolling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85US-0732531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86EP-0303210
                                                                                  84DD-0262804.
                                                                                                    84DD-0262804
                                                                                                                                                                                                                                          protein; 10
                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                              Handel L;
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                                                                                                                                                                                                                                                                                                                                     Score 63; DB 7;
Pred. No. 0.00012;
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                                                                                                                                                         analogue; peptide synthesis;
fertility;
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RESULT
AAP70922
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RESULT
AAP60576
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Best Local Similarity
Matches 10; Conserv
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Best Local :
                                                                                                                                                                                                                (TULA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The gonadotropin releasing hormone and its analogues are prepd. by a new multistage rapid peptide synthesis method in soln., where the intermediates are not isolated. The process is rapid and gives very pure peptide quickly and using little equipment. The peptide can be used in veterinary medicine to synchronise ovulation in large animal herds, and in human medicine in the treatment of fertility disorders.
                                                                                                Sequence
                                                                                                                   Peptide inhibits the release of lutenising See also AAP60575.
                                                                                                                                                  Disclosure; Page 990; 5pp; Japanese.
                                                                                                                                                                                                                                                23-AUG-1984;
                                                                                                                                                                                                                                                                                         18-SEP-1986.
                                                                                                                                                                                                                                                                                                              JP61210098-A
                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                      Lutenising
                                                                                                                                                                                                                                                                                                                                                                           Novel decapeptide with LHRH inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                     AAP60576;
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP60576 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; page 7; 8pp; german
                                                                                                                                                                      Deca:peptide - inhibits LH-RH hormone release
                                                                                                                                                                                           WPI; 1986-321434/49.
                                                                                                                                                                                                                                                                    23-AUG-1985;
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1 EHWSYGLRPG
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| ehwsyglrpg
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1 ehwsyglrpg 10
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TULANE E FUND ADMINISTRA.
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                                                                                                10 AA;
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                                             Conservative
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Pred. No.
                                                       Score 63;
Pred. No.
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                                            Mismatches
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                                           . 0.00012; ches 0;
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                                                                DB 7;
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                                                                                                                                                                       activity
                                                              Length 10;
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AAP70922 standard; peptide;

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RESULT
AAP90630
ID AAP9
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHRH; contraception; precocious puberty; endometriosis; breast tumours; prostate tumours; ectopic tumours; meno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Luteinising hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic
                                                                                                                                                                                                                                                                                                    This luteinising hormone releasing hormone (LHRH) agonist has either a kecomethylene or dihydroketomethylene gp. replacing the amide linkage between residues 9 and 10 in LHRH. This results in an increase in oral activity. It is useful for eg male and female contraception, treatment of precocious puberty and endometriosis and treatment of breast—and prostate tumours.
                                                                                                                                                                                                                                                                                                                                                                                                      Orally active luteinising hormone-releasing hormone peptide analogues - have keto:methylene or hydroxy:ethylene in place amide between proline(9) and glycine(10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1985;
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                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; page 4; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1987-334627/47.
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                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                             See also AAP70923-27.
                                                                                       AAP90630;
         Luteinizing hormone releasing hormone (LHRH); LHRH antagonist; 19-nor-progestational agent; female gynaecological disorders.
                                          Sequence of
                                                                  14-JUN-1989
                                                                                                              AAP90630 standard;
                                                                                                                                                                     \vdash
                                                                                                                                                                                           1 EHWSYGLRPG
                                                                                                                                    8
                                                                                                                                                                     ehwsyglrpg
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                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                        10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative 0
                                           luteinizing hormone releasing hormone (LHRH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olsen CM;
                                                                   (first entry)
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    methylene(Gly)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "other= pyroglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= other
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                                                                                                               protein;
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                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hormone agonist
                                                                                                                                                                                                                   Score 63; DB 8; pred. No. 0.00012; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ectopic tumours; menopause.
                                                                                                                                                                                                                                           Length 10;
                                                                                                                                                                                                                       Indels
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Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP301850-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vickery BH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYNT ) SYNTEX (USA) INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              steroid producn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compsn. comprising LHRH-antagonist and 19-nor progestational for treating female gynaecological disorders based on gonads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-033720/05
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                    AAR15713;
                                                                                                                                                                                                                                                                                        AAR15713
                                                                                                                                                                                                                                               24-JAN-1992
                                                                                                                                                       Key
Modified-site
                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                           Peptide #1
                                                                                                                                                                                                         luliberin.
                     22-APR-1991;
                                                             W09116343-A.
                                                                                                    Modified-site
                                                                                                                         Modified-site
                                         31-OCT-1991.
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                                                                                                                                                                                                                                                                                                                                        ehwsyglrpg 10
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                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                              with homology to LHRH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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                       91WO-FR00332
                                                                                                                                                                  Location/Qualifiers
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                                                                                   /note=
                                                                                              /label= OTHER
                                                                                                                ′label= Hyp
                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                          Protein; 10 AA
                                                                                   "amidated"
                                                                                                                                    "pyroGlu"
                                                                                                                                                OTHER
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                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 10;
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23-APR-1990;

90FR-0005147

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RESULT 1
AAR26819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The C-terminal residue (Gly-CO-NH2) can be replaced by ethylamide. This peptide and fragments of it (i.e. amino acids 4-10, 5-10, 6-10 and 7-10) are agonists and antagonists of LHRH. They are useful for treating e.g. precocious or delayed puberty, psychiatric disorders esp. those of the libido or sexual aggression, etc. In addition they are useful for functional exploration of the hypothalamus hypophyseal are useful for functional exploration of the hypothalamus hypophyseal axis and for radioimunological or biological assay (of LH, FSH and
      New deca:peptide luteinising hormone-releasing hormone antagonists - for treating precocious puberty, hormone dependent tumours, endometritis, cystic diseases; also as contraceptive
                                                                                                                                                                                                                                                                                                                                          Luteinising hormone; LHRH; hypothalamic; antiovulatory; tumours; antineoplastic; precocious puberty; ovulation; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR26819 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    steroid levels) in biological fluids and biopsy samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide homologous with luteinising hormone-releasing hormone used to treat gynaecological conditions, cancer of gonads and sec. sexual organs, psychiatric conditions and in assays
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                                                                                                                                      30-JAN-1991;
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                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                  LH releasing
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                                                                                                            (TULA ) TULANE EDUCATIONAL FUND.
                                                                                                                                                                                                                 W09213883-A
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1 ehwsyglrpg 10
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                                                                                  Juhasz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 AA;
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                                                                                                                                     910S-0647786.
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                                                                                                                                                                                                                                                                 /label- pGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide;
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                                                                                    Schally AV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63; DB 12;
Pred. No. 0.00012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which possesses high antiovulatory and antineoplastic activity, is
if free of anaphylactoid side effects and is believed to be free of
endematogenic effects. The peptide may be used to treat precocious
puberty, hormone dependent tumours, e.g. malignant and benign
overstate tumours, e.g. secondary amenorrhoea, endometriosis and
covarian and mammary cystic diseases. The peptide is also useful
for regulating ovulation e.g. as precoital or postcoital
contraceptives, for synchronising oestrus in livestock and for
improving the "rhythm" method. It is also useful for regulating
the human menopausal gonadotropin, follicle stimulating and LH levels
the human menopausal and postmenopausal periods. As it suppresses
the spermatogenesis and testosterone levels in males, it may be of
cotential use for male contraception.

See also AAR26818, AAR29046-7.
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Best Local S
Matches 10
                                                                                                                                                                                                        (LADD/) LADD A I
(WANG/) WANG C I
(ZAMB/) ZAMB T.
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                                                                                                                                                  WPI; 1994-357910/44.
                                                                                                                                                                                                                                                               27-APR-1993;
14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                            WO9425060-A.
                                                                                                                                                                                                                                                                                                                                                                                                                androgen-dependent carcinoma; antitumour; infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Helper T cell epitope; universal immune stimulator; invasin; hapten;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHRH hapten for attachment to universal immune stimulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR62689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR62689 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                     28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                          Immunogenic luteinising hormone releasing hormone peptide(s)
that suppress LHRH activity in males and females
                                                                                                                                                                                                                                                                                                                                 10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           decapeptides is an antagonistic analogue of hypothalamic LHRH
                                                                                                                                                                              ΑE
                                                                               Page 104;
                                                                                                                                                                                                                                                                                                                                                                                                                               LHRH;
                                                                                                                                                                           Wang
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nilarity 100.
Conservative
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94US-0229275.
                                                                                                                                                                                                                                                                                                     94WO-US04832
                                                                                                                                                                                                                                                                                                                                                                                                                               luteinising
                                                                                                         activity in
                                                                             213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
                                                                                                                                                                               Zamb
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                                                                                                                                                                                                                                                                                                                                                                                                                             hormone releasing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63; DB 13;
Pred. No. 0.00012;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                               hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                             prostate;
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Synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or cytotoxic T lymphocyte eptide or giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th)

0;

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cc a heterogeneous population expressing diverse HLA phenotypes, and (B) cc an adjuvant peptide sequence from the invasin protein of Yersinia. cc spacer amino acid sequences (e.g. Gly-Gly) can be provided between the components in the hapten is LHRH, then optionally the invasin domain cc can be omitted from the immune stimulator and hapten cc attached to the stimulator to provide a potent vaccine for attached to the stimulator to provide a potent vaccine for cutering e.g. prostatic hyperplasia, androgen-dependent carcinoma, co cuterine tumours, recurrent functional ovarian cysts, (severe) cc induction of infertility.
RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                            gonadorein
                                                                                                                                                                                                                                                                                                                                                                                                            LHRH peptide
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                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                    luteinising hormone releasing hormone; follicle stimulating; FSH;
                                                                                                                                                       Gauthier
                                                                                                                                                                                                   06-MAY-1988;
                                                                                                                                                                                                                       06-MAY-1988;
                                                                                                                                                                                                                                            25-APR-1995
                                                                                                                                                                                                                                                                                                                        Modified-site
A new method is provided for preparing a decapeptide of formula pGlu-His-Trp-Ser-Tyr-Xaa-Leu-Arg-Pro-Gly-NH2, in which a protected nonapeptide corresponding to the N-terminal of the peptide is first prepared on a benzhydrylamine resin, the Pro residue being attached
                                                                                    prepn. of luteinising hormone and follicle stimulating hormone
releasing peptide(s) - by cleaving a protected nona peptide resin
by photolysis to remove the support, coupling with glycinamide and
                                                                                                                                                                           (BOEH ) BIO-MEGA/BOEHRINGER INGELHEIM RES
                                                       Claim 1; ; 18pp;
                                                                            deprotecting
                                                                                                                                   WPI;
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10; Conser
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                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
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                                                                                                                                                                                                                                                                                                              "pyroglutamic acid"
                                                                                                                                                                                                                                                                                          "Gly-NH2"
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. 0.00012;
ches 0;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-OCT-1992;
14-DEC-1990;
14-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gonadotropin releasing hormone; GnRH; motility disorder; functional bowel disease; leuprolide acetate; luteinising hormone; progesterone; relaxin; autonomic nervous system; drug delivery; there irritable bowel syndrome; diabetes; scleroderma; Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gonadotropin
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This sequence represents naturally occuring gonadotropin releasing hormone (GnRH). Analogues of GnRH are represented by AAR86846-56.

Motility disorders, including functional bowel disease, can be treated by the administration of one of the GnRH analogues shown here (e.g. by the administration of one of the GnRH analogue inhibiting leuprolide acetate). This is due to the GnRH analogue inhibiting production of reproductive hormones such as luteinising hormone, progesterone and relaxin. Motility disorders are caused from progesterone and relaxin attonomic nervous system. Due to this, the GnRH abnormalities of the autonomic nervous system.
                                                                                                                                                                                                                                                                           Treating motility disorders associated with systemic lupus erythematosus - by admin. of gonadotropin releasing hormon analogue, to control nausea, vomiting, abdominal pain etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5434136-A
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                                                                                                                                                                                                                          Disclosure; Column 3; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-263259/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mathias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MATH/)
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Conservative
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90US-0626402.
91US-0744977.
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Pred.
                                                                                                                                                                                                                                                                                        gonadotropin releasing hormone
vomiting, abdominal pain etc.
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RESULT J
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analogues may also exert effects on the autonomic nervous system. The GORH analogues are administered by injection (which may be intavenous, subcutaneous or intramuscular), or by a drug delivery system. The drug delivery system can comprise a drug implant with timed release, a nasal spray or an injection of a long-lasting depo form. This method is used to alleviate symptoms such as nausea, vomiting, abdominal pain and altered bowel habits. The sequences can be used to treat motility disorders in a wide variety of other diseases including irritable bowel syndrome, diabetes, scleroderma and Parkinson's disease.
                                                                                                                                           8 Different forms of GnRH (given in AAR75152-59) have previously been isolated from vertebrate species. A precursor for an additional form of GnRH, (Ser8)-GnRH (AAR75151), has now been
                                                                                                                                                                                                                         New gonadotropin releasing hormone preprohormone DNA - used to develop prods. for regulation of reproductive function and diagnosis of reproductive capacity and disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gonadotropin releasing hormone; GnRH; gonadoliberin; reproduction; transgenic animal; transgenic fish; transgenic fowl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gonadotropin
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                                                                                                                                                                                               Disclosure; Fig.la; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-1995.
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                                                                                                       Sequence
                                                                                                                                                                                                                                                                                 WPI; 1995-185526/24.
                                                                                                                                                                                                                                                                                                          Adelman JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9512309-A1
                                                                                                                                                                                                                                                                                                                                  (STRD ) UNIV LELAND STANFORD JUNIOR. (UYOR-) UNIV OREGON HEALTH SCI. (UYOR-) UNIV OREGON STATE.
                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-1993;
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1 EHWSYGLRPG 10
                                     l Similarity 100
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                                                                                                                                                                                                                                                                                                         Fernald RD
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                                     Score 63; DE
Pred. No. 0.0
0; Mismatches
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Pred. No. 0.00012;
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Search completed:
Job time: 87 sec
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Matches 10
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16-SEP-1992;
07-NOV-1994;
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                                                                                                                                                                The invention relates to the obtaining of a potent agonist or antagonist peptide by the replacement of selected amino acids with synthetic achiral amino acids. The present sequence represents a luteinising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gonadoliberin
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                                                                                                                                      Sequence
                                                                                                                                                                                                        Disclosure; Columns 11-12; 15pp; English.
                                                                                                                                                                                                                         New bradykinin analogues contg. N-benzyl-glycine -bradykinin agonists or antagonists, useful e.g. as
                                                                                                                                                                                                                                                         WPI; 1996-299898/30.
                                                                                                                                                                                                                                                                           Mitchell AR,
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                                              1 EHWSYGLRPG
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                                                                                       Conservative
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                                                                                                                                                                                                                                                                                              CALIFORNIA
           November 13,
                                                                                                                                      ΑA;
                                                                                                                                                                                                                                                                          Young JD;
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92US-0945664.
94US-0335202.
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                                                                                                                                                          hormone
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           2001, 14:27:41
                                                                                                                                                          (LHRH).
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Pred. No.
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                                                                                       Indels
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Minimum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/pcodata/2,
2: /ggn2_6/pcodata/2,
3: /cgn2_6/pcodata/2,
4: /cgn2_6/pcodata/2,
5: /ggn2_6/pcodata/2,
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Copyright (c) 1993 - 2000 Compugen
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US-08-448-488-22
US-08-446-692-1
US-08-488-351A-1
US-08-488-351A-1
US-08-488-351A-1
US-08-488-351A-1
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US-08-124-491-18
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US-08-912-118-13
US-08-912-314A-11
US-08-912-314A-11
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Sequence 2
Sequence 3
Sequence 1
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77, Appl
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| Query Match Best Local Sin Matches 10; | RESULT 1 Sequence 9, Application US/07714540 Sequence 9, Application US/07714540 Patent NO. 5263521 GENERAL INFORMATION: APPLICANT: Almquist, Ronald G. APPLICANT: Toll, Lawrence TITLE OF INVENTION: ENZYME AND NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESSEE: Irel1 & Manella STRRET: 545 Middlefield Road, CITY: Menlo Park STATE: California COUNTRY: USA ZIP: 94025 COMPUTER READABLE FORM: MEDIUM TYRE: Plappy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS- SOTWARE: PatentIN Release #1 CURRENT APPLICATION NUMBER: US/07/714 FILLING DATE: 19910607 CLASSIFICATION: NAME: Reed, Dianne E. NAME: Reed, Dianne E. REGISTRATION NUMBER: 31,292 REFERENCE/DOCKET NUMBER: 8500 TELECOMMUNICATION INFORMATION: NAME: Reed, Dianne E. REGISTRATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LEANTH: 10 amino acids TYPE: AMINO ACID STRANDEDNESS: LINGAR HOLD STAPE: 10 amino acids TYPE: AMINO ACID STRANDEDNESS: 11naar HOLD CULE TYPE: Protein | 5 5 6 5 6 5 6 5 6 5 6 5 6 5 6 5 6 5 6 5 |
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| 100. Similarity 100. 0; Conservative | -9 Application US/0 5262521 FORMATION: FORMATION: TOLL LAWFERCY INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INCLUDENCE ADDRESS: SEE: IT Fell & Man INGENCE ADDRESS: SEE: IN Fell & Man INGENCE ADDRESS: SEE: INFORMAT 94025 REALDALE Menlo Park California Y: USA 11 FORM 94025 READBALE FORM: TYPE: Floppy di ING SYSTEM: FO-D REE Patentin Real ING SYSTEM: FO-T REE PATENTION DATA: ATION NUMBER: USA ATION NUMBER: ATION NUMBER: ATION NUMBER: ATION NUMBER: ATION NUMBER: 30 AGENT INFORMAD NEC/DOCKET NUMBER: 30 AGENT INFORMAD ONE: 415-327-725 Y. 415-327-725 Y. 415-327-725 TOG141 N FOR SEQ ID NO: CHARACTENISTICS: 10 amino acids DATION ACID EDNESS: 11 amino acids DATOR: POR SEQ ID NO: CHARACTERISTICS: 11 amino acids DATOR: Single GY: Jinear TYPE: Protein | |
| 100.0% 100.0% ive | n US/0771454 t, Ronald G. awrence ISOLATED A ENSYME AND: 1 13 18 ESS: 6 Manella lefield Road a lefield Road a lefield Road a lefield Road a b COMPATION: PCLOS/MS IN Release # DATA: COMPATION: RATION: RATI | 2025 205 206 207 208 208 208 208 208 208 208 208 208 208 |
| ; Score 63; DB 1; Length ; Pred. No. 7e-05; 0; Mismatches 0; Indel | 4540 4540 G. D ATRIAL PEPTIDE-DEGRADING AND NOVEL COMPOUNDS USEFUL a boad, Suite 200 Version #1.25 7714,540 922 98500-0135.00 N: | US-08-302-915-2 US-07-690-983D-22 US-07-690-983D-24 US-07-690-983D-14 US-07-690-983D-14 US-07-690-983D-14 US-07-690-983D-18 US-07-690-983D-18 US-07-690-983D-28 US-07-690-983D-28 US-07-690-983D-28 US-07-690-983D-28 US-07-690-983D-40 US-07-690-983D-40 US-07-690-983D-40 US-07-690-983D-47 US-08-446-692-17 US-08-446-692-17 US-08-448-351A-17 US-08-448-351A-12 US-08-448-351A-12 US-08-448-351A-12 US-08-448-351A-12 |
| 10; | AS IN | sequence |
| 0; Gaps 0;. | INHIBITORS THEREOF | 10ce 2, Applice 22, Applice 24, Applice 30, Applice 14, Applice 18, Applice 18, Applice 20, Applice 20, Applice 20, Applice 40, Applice 40, Applice 41, Applice 41, Applice 47, Applice 17, Applice 17, Applice 17, Applice 17, Applice 29, Applice 20, Applice 29, Applice 20, Applice 20, Applice 29, Applice 20, Applice 20 |

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US-07-690-983D-2

Floppy disk

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Sequence 2, Application US/07690983D Patent No. 5403586
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Best Local Similarity
Matches 10; Conserv
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patent No. 5403586
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TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: STEWART, Andrew G. APPLICANT: TSONIS, Con G. TITLE OF INVENTION: FUSION PROTEINS NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/AU90/00373
FILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                          APPLICANT: RUSSELL-JONES, Gregory J.
APPLICANT: STEWART, Andrew G.
APPLICANT: TSONIS, CON G.
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C.
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                COUNTRY:
                                                                               ADDRESSEE:
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GY: unknown
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                                                               3000 K Street, N.W.
                                                                                   Foley & Lardner
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Best Local Similarity
Matches 10; Conser
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APPLICATION UMBER: PCT/AU90/
FILING DATE: 24-AUG-1990
ATTORNEY_AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2021672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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COMPUTER: II
                                                  FILING DATE: 17-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,495
FILING DATE: 09-NOV-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                            STREET: 727 Twer
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                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                            APPLICATION NUMBER: US/08/343,883 FILING DATE: 17-NOV-1994
                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                   APPLICATION NUMBER: FR 9 FILING DATE: 01-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Application US/08343883 5573767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 10 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                 Virginia
                                                                                                                                                                                                                                                                                                                                                                  : Larson and Taylor
727 Twenty-Third Street, South
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dufour, Raymond J.
Roulet, Claude J.M.
Chouvet, Claire D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonneau, Michel B.

WENTION: Method for improving the organoleptic VENTION: Method for improving the organoleptic VENTION: qualities of the meat from uncastrated male domestic VENTION: animals, vaccines which are usable in this method, new VENTION: peptide, in particular for producing these vaccines...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-1991
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                                         FR 9102513
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Pred. No. 7e-05;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids

APPLICATION NUMBER: FR 9115289 FILING DATE: 10-DEC-1991

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Best Local Similarity
Matches 10; Conserv
                                                         ZIP: 2007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/000,931
FILING DATE: 05-JAN-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08000931
Patent No. 5578477
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICANT: Tamanol Dr., Fuyuhiko
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF
TITLE OF INVENTION: INHIBITORS OF PROTEIN FARNESYLTRANSFERJ
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION: /le
OTHER INFORMATION: /nc
PUBLICATION INFORMATION:
               ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EATURE:
                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide LOCATION: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS:
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
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G. Nair, R. M.
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64098/102/ARDE
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Pred. No.
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                                                                                                                                                                                                                                                          Suite 500
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US-08-428-488-22

; Sequence 22, Appli

; Patent No. 5624894
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NAME/KEY: Modified-site LOCATION: 10 COATION: 10 COATION: /note 128-488-22
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids TYPE: amino acid STRANDEDNESS: single
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Best Local Similarity
Matches 10; Conserv
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: PE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary F
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                      FEATURE:
NAME/KEY:
                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/O FILING DATE: 27-APR-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                   NAME: Baumeister, Mary Katherine REGISTRATION NUMBER: 26,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States ZIP: 22313-1404
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STATE: Virginia
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                                                                                    OTHER INFORMATION:
                                                                                                        LOCATION:
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                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRAIN-ENHANCED DELIVERY OF NEUROACTIVE PEPTIDES BY SEQUENTIAL METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.
                /note= "Position 10 = Gly-NH2."
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                                                                                     "Position 1 -
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LOCATION: 10
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-341-219-11
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Best Local Similarity
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Query Match
Best Local Similarity
Matches 10; Conserv
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sherwood, N.
APPLICANT: Gothhlf, Y.
TITLE OF INVENTION: Compounds and
TITLE OF INVENTION: Reproduction
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                            TOPOLOGY: unk
MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: COruzzi,, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: N V
                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
LOCATION: 1
                                                                                                                                                                                                                                                                                              ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coruzzi,, Laura A. REGISTRATION NUMBER: 307
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                                                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRY: USA
10036-2711
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                           10 amino acids
 100.0%; milarity 100.0%; Conservative 0;
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NO
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                                                                                                                                                                                                /product= "OTHER"
/label= Glu1
/note= "=pyroglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/341,219
                                                                                                   /product= "OTHER"
/label= Gly10
/note= "amidated"
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            0
                         Score 63; DB 1;
pred. No. 7e-05;
            Mismatches
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                                            DB 1;
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                                          Length 10;
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                 Gaps
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                    0;
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US-08-453-588-22
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US-08-453-588-22
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                                                                                                                                                                                                     US-08-591-917-1
                                                                                                                                                                                                                                                                     Дb
                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                   Sequence 1, Application US/08591917 Patent No. 5707964
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/078,66
ETLING DATE: 16-JUN-1993
ETLING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: MARY E. GOTMLEY
REGISTRATION UNMBER: 34,409
TELECOMMUNICATION INFORMATION:
                                                                  GENERAL INFORMATION:

APPLICANT: Nett, Torrance M
APPLICANT: Nett, Torrance M
APPLICANT: Glode, Leonard Michael
APPLICANT: Glode, Leonard Michael
TITLE OF INVENTION: A METHOD FOR TREATING CANCER
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anna van der Zee, Irma Marianne van Die, APPLICANT: Willem Pieter Martin Hoekstra, APPLICANT: Josephus Theodorus Gielen. APPLICANT: Josephus Theodorus Gielen. TITLE OF INVENTION: Carrier system against GnRH NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: AKZO NO. 5684145el Patent Department STREET: 1300 Piccard Drive, Suite 206 CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 30-MAN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                   1 EHWSYGLRPG 10
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            STATE:
                                         STREET:
                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                      1 EHWSYGLRPG 10
                                                                                                                                                                                                                                                                                                                                    10;
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                    SSEE: Sheridan Ross & McIntosh
T: 1700 Lincoln Street, Suite 3500
Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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            Colorado
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                                                                                                                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative
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16-JUN-1993
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30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258-5200
                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 7e-05;
Mismatches
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Gaps

COMPUTER READABLE FORM:

COUNTRY: U ZIP: 80203

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RESULT 10
US-08-446-692-1
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Best Local S
                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MARIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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GENERAL INFORMATION:
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: KOVARIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ladd, Anna APPLICANT: Wang, Chang Yi APPLICANT: Zamb, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 100.0%; Score 63; DB 1; Length 10; Local Similarity 100.0%; Pred. No. 7e-05; nes 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 10154-0053
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amino acid
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                                                                (212)415-8745
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RESULT

US-08-694-865-18

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Best Local Similarity
Watches 10; Conserve
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US-08-796-598-6
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                                                             Matches
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                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                               TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,598
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/446,055
RIFLING APPLICATION NUMBER: US 08/446,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PATTERSON, DALE H.
APPLICANT: TARR, GEORGE E.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: SY TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: FLYNN Esq., Kerry A
REGISTRATION NUMBER: 33,69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: High
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Patent Administrator - Testa, Hurwitz & ADDRESSEE: Thibeault
                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-MAY-1995
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1 EHWSYGLRPG 10
                            1 EHWSYGLRPG 10
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5. 5827659
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                                                            Conservative
                                                                                                                                                                      SS: single
linear
                                                                                                                                                                                                                                                                                    (617) 248-7000
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                                                                                                                                                         peptide
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                                                                           100.0%; Score 63; DB 2; 100.0%; Pred. No. 7e-05;
                                                                                                                                                                                                                                                                                                                                33,693
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Pred. No. 7e-05;
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                                                                                        Length 10;
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OTHER INFORMATION: /note= "This position is pyroGlu." US-08-694-865-18
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US-08-488-351A-1
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Best Local Similarity
Transparents 10; Conser
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                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08488351A Patent No. 5843446
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                   GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELECHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1
                                                                                                                                              APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: PALO ALTO
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site LOCATION: 1
                                                                            CITY: New York
STATE: NY
                                                                                                        ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EHWSYGLRPG 10
                                                                                                                                                                                                                                                                                                                                                                                                                 EHWSYGLRPG 10
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                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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MOLECULE TYPE: peptide US-08-488-351A-1
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Patent No. 5843901
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MATIA C.H. Lin 29,323
REGEISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATA:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/(
APPLICATION NUMBER: 27-APR-1992
474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 7-JUN-1
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 08/229,275
APPLICATION NUMBER: 14-APR-1994
FILING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS: LAHIVE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROESKE, ROGER W.
TITLE OF INVENTION: LHRH Antagonist Peptides
                 NAME: DECONTI INFORMATION:
NAME: DECONTI, GIULIO A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-007
TELECOMMUNICATION INFORMATION:
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                                                                                       APPLICATION NUMBER: US/08/480,494B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
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Pred. No. 7e-05;
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ZIP: 02110

ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,175A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 422
ATTORNEY/AGENT IMFORMATION:
NAME: RAUSCHENBACH, Kurt
REGISTRATION NUMBER: 40,137
REFERENCE/DOCKET NUMBER: SYP-114
TELECOMMUNICATION IMFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7000
INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                             Query Match 100.0%; Score 63; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 7e-05; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08447175A Patent No. 5869240
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APPLICANT: PATTERSON, DALE H.

APPLICANT: PATTERSON, DALE H.

TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
TITLE OF INVENTION: SPECTROMETRY.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: High
CITY: Boston
STATE: MA
1 EHWSYGLRPG 10
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1 EHWSYGLRPG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EHWSYGLRPG 10
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Search completed: November 13, 2001, 14:26:49 Job time: 35 sec

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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       PIR_68:*
1: pir1:
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4: pir4:
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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      Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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| RESULT 2 RHSHG GUARDAN Sci. U.S.A. 69, 278-282, 1972 A. Wither Drimary structure of the counce hope that a fee or the counce has a fee or the counce hope that a fee or the counce has a fee or the counce hope that a | 9; Conservative 1 EHWSYGLRPG 10 : QHWSYGLRPG 10 | essential for biological activity chormone stimulates the secretion of both of the secretion of chormone stimulates the secretion of both of the secretion of both of the secretion of the secret | hally, A.V. un. 45, 483-487, 1971 un. 45, destroyers and FSH-releasing residue in porcine LH and FSH-releasing MUID:72117544 | M.G.; Schally, A.V. 822-827, 1971 H- and FSH-releasing hormone by t 065376 ormones have the same physicochem | R; Baba, Y; Matsuo, H.; Schally, A.V. R; Baba, Y; Matsuo, H.; Schally, A.V. Biochem. Biophys. Res. Commun. 44, 459-463, 1971 A; Title: Structure of the porcine LH- and FSH-releasing hormone. II. A; Reference number: A90172; MUID:72114303 A; Accession: A01411 | tica (domestic pig) ce_revision 13-Jul-1981 #text_change 18 | ALIGNMENTS | 30 42 66.7 828 2 T08556 hypotheting specific spe |
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| shee nge 1 Rivi | | y on of both luteinizing and roglutamic acid experimental eximental | rmone. | none by the solid-phase me sicochemical and biologic | II | | | hypothetical prote aldose reductase h hypothetical prote yabN protein - Esc probable transport conserved hypothet cellulase (EC 3.2. serine proteinase hypothetical 3/45 p probable fmu prote hypothetical prote hypothetical prote anglogenesis inhib hypothetical prote anglogenesis inhib hypothetical prote hypothetical prote anglogenesis inhib hypothetical prote anglogenesis inhib hypothetical prote |

A; Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing fa A; Reference number: A93780; MUID: 72094314 A; Accession: A93780

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the same biological activity the secretion of both luteinizing

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A; Molecule type: protein
A; Residues: 1-10 < BUR>
A; Residues: the natural and synthetic hormones have the same biological activity
A; Note: the natural and synthetic hormones the secretion of both lutein
C; Comment: This hypothalamic hormone stimulates the secretion of both lutein
C; Superfamily: gonadoliberin
C; Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
C; Keywords: amidated carboxyl end; doll #status experimental
F; 1/Modified site: pyrrolidone carboxyl end (Gly) #status experimental
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N;Alternate names: luteinizing hormone releasing hormone
                                                                                                                                                         gonadoliberin precursor - African clawed frog gonadoliberin precursor - African clawed frog N;Alternate names: luteinizing hormone releasing hormone (Species: Xenopus laevis (African clawed frog) (C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999 (C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999 (C;Date: 13-Sep-1996 #settey, J.F. Ridges, W.P.; Wray, S.; Battey, J.F. Rendocrinology 134, 1835-1845, 1994 Rendocrinology 134, 1835-1845, 1994 Rendocrinology 134, 1835-1845, 1994 Rendocrinology 134, 1835-1845, 1994 Rendocrinology 134, 1835-1845, MUID:94185563 A;Reference number: I51423; MUID:94185563 A;Reference number: I51423; MUID:94185563 A;Reference number: I51423; MUID:94185563 A;Reference preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-89 <4RAY) A;Molecule type: DNA A;Residues: 1-89 <4RAY)
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9; Conserv
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9; Conserva
   Similarity
9; Conser
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90.0%;
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90.0%;
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90.0%;
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         score 60; DB
Pred. No. 0.00
1; Mismatches
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Pred. No. 0.0017;
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0.00022;
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0.0022;
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EHWSYGLRPG

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gonadoliberin precursor - mouse
y,Alternate names: gonadotropin-releasing hormone (GnRH); luteinizing hormone
N;Contains: gonadoliberin; gonadoliberin-associated protein (GAP)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 18-Mar-1997 #text_change 18-Jun-1999
C;Accession: A47578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: gonadoliberin stimulates pituitary secretion of lu A; Note: gonadoliberin-associated protein may have prolactin relea C; Superfamily: gonadoliberin (C; Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglu F; 1-23/Domain: signal sequence #status predicted <SIG>F; 1-23/Domain: signal sequence #status predicted <GLB>F; 22-31/Product: gonadoliberin #status predicted GLB>F; 22-31/Product: gonadoliberin associated protein #status predict. F; 32-Modified site: pyrrolidone carboxylc acid (Gln) (in mature: F; 32/Modified site: amidated carboxyl end (Gly) (amide in mature: F; 31/Modified site: amidated carboxyl end (Gly) (amide in mature: F; 31/Modified site: amidated carboxyl end (Gly) (amide in mature: F; 31/Modified site: amidated carboxyl end (Gly) (amide in mature)
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A;Accession: A47578
A;Molecule type: DNA
A;Residues: 1-90 <MASS
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C;Genetics:
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                                                     A; Molecule type: mRNA
A; Residues: 1-92 <ADE>
A; Residues: 1-92 <ADE>
A; Cross references: GB:M12578; NID:g183418;
A; Experimental source: hypothalamus
R; Seeburg, P.H.; Adelman, J.P.
Rature 311, 666-668, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-92 <HAY>
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A; Title: Characterization of cDNA for precursor A; Reference number: A93342; MUID:85012739
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C;Function:
A;Description: gonadoliberin stimulates pituitary secretion of lutropin and follitropin A;Description: gonadoliberin associated protein may have prolactin release inhibiting activity C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid F;1-23/Domain: signal sequence **status predicted <SIG>F;24-92/Product: progonadoliberin *status experimental <MAT>F;24-93/Product: gonadoliberin *status experimental <MAT>F;24-792/Product: gonadoliberin *status experimental <MAT>F;24-792/Product: gonadoliberin *status experimental <MAT>F;34/Modified site: amidated carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from following carboxyl end (Gly) (amide in mature form from
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A;Accession: A93342
A;Molecule type: mRNA
A;Residues: 1-15,'S',17-92 <SEE>
A;Cross references: GB:X01059; NID:g34356; PIDN:CAA25526.1; PID:g34357
A;Experimental source: placenta
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A;CrOSs-references: GDB:133746;
A;Map postition: 8p21-8p11.2
A;Introns: 47/3; 79/3
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A;Contents: annotation; degradation pathway of synthetic hormone
                                                                                                                                                                                                                                                 R;Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Se Proc. Natl. Acad. Sci. U.S.A. 83, I79-183, 1986 A;Title: Isolation of the gene and hypothalamic A;Reference number: A94090; MUID:86094338 A;Accession: B26173
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A;Title: The chemical identity of the immunoreactive
A;Reference number: A90108; MUID:83126573
                                                                   A;Cross-references: GB:M12579; NID:g204445; PIDN:AAA41263.1; R;Maler, C.C.; Marchetti, B.; LeBoeuf, R.D.; Blalock, J.E. Cell. Mol. Neurobiol. 12, 447-454, 1992
                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-92 <BON>
A;Cross-references: GB:M31670; NID:g204447; PIDN:AAA41264.1;
A;Cross-references: GB:M31670; NID:g204447; Seeburg, P.H.
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                                                                                                  gonadoliberin I precursor - chicken N;Alternate names: gonadotropin-releasing C;Species: Gallus gallus (chicken) C;Date: 21-Feb-1997 #sequence_revision 21-C;Accession: I50644; S33507 R;Dunn, I.C.; Chen, Y; Hook, C.; Sharp, P. J. Mol. Endocrinol. 11, 19-29, 1993 A;Title: Characterization of the chicken p. A;Title: Characterization of the chicken p.
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C; Genetics:
                                 A;Reference number: I50644; MUID:94059355
A;Accession: I50644
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#text_change

16-Jul-1999

hormone

P.J.;

Sang,

preprogonadotrophin-releasing

hormone-I

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A;Description: stimulates pituitary secretion of lutropin and follitropin A;Note: gonadoliberin-associated protein may have prolactin release inhibiting activi C;Superfamily: gonadoliberin (C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid F;1-23/pomain: signal sequence #status predicted <SIG>F;24-92/product: progonadoliberin #status predicted <PN>F;24-93/product: gonadoliberin #status predicted <GLN>F;24-93/product: prolactin release-inhibiting factor #status predicted <PIF>F;37-92/product: prolactin release-inhibiting factor #status predicted <PIF>F;33/Modified site: amidated carboxyl end (Gly) (amide in mature form from following F;33/Modified site: amidated carboxyl end (Gly) (amide in mature form from following
                                                                                                                                                                                 C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic ac
F;L/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-92 <MAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: gonadotropin-releasing hormone I
C;Species: Alligator mississippiensis (American alligator)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-10 <LOV>
                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A60066; MUID:91352338 A; Accession: A60066
                                                                                                                                                                                                                                                                                                                                                                                                          Regul. Pept. 33, 105-116, 1991
A;Title: Primary structure of two forms of
                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lovejoy, D.A.; Fischer, W.H.; Parker, Regul. Pept. 33, 105-116, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: thymus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: A60066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gonadoliberin I - American alligator
                                                                                                        Query Match
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                                                                            Local
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1 EHWSYGLRPG
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                                                  Similarity
8; Conser
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                                                     Conservative
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90.0%;
                                                                            88.9%;
                                               Score 56; DB
Pred. No. 0.00
2; Mismatches
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Pred. No. 0.0023;
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                                                                      DB 1;
0.0011;
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RHILLS

gonadoliberin I precursor - sharptooth catfish
N;Alternate names: gonadoliberin; catfish-type; gonadotropin-releasing hormone I (GnRH-I
N;Contains: gonadoliberin I; gonadoliberin I-associated protein form I; gonadoliberin I-
N;Contains: gonadoliberin I; gonadoliberin I-associated protein form I; gonadoliberin I-
C;Species: Clarias gariepinus (sharptooth catfish)
C;Species: Clarias gariepinus)
C;Species: Clarias gariepinus (sharptooth catfish)
C;Species: Clarias gariepinus)
C;Species: Clarias gariepinus
C;Species: Clarias gariepin
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A; Residues: 1-92 < DUZ>
A; Cross references: EMBL:X69491;
C; Genetics:
A; Introns: 47/3; 79/3
C; Superfamily: gonadoliberin
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Proc. Natl. Acad. Sci. U.S.A. 92, 8363-8367, 1995

A;Title: Three gonadotropin-releasing hormone genes in one organism suggest novel roles
A;Reference number: 150739; MUID:95396797

A;Recession: I50739
A;Rocession: T50739; MUID:95396797
A;Rocession: T50739
A;Rocession: T5073
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C;Species: Haplochromis burtoni
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 150739
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Best Local
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8; Conserv
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8; Conser
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80.0%;
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pred. No. 0.026;
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A; Experimental source: brain
C; Superfamily: gonadoliberin
C; Superfamily: gonadoliberin
C; Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
C; Keywords: asignal sequence #status predicted <STG>
F; 1-21/Domain: signal sequence #status predicted <STG>
F; 2-31/Product: gonadoliberin I *status experimental <MAT1>
F; 35-80/Product: gonadoliberin I -associated protein #status predicted <MAT2>
F; 35-80/Product: gonadoliberin I -associated protein #status form) #status
F; 22/Modified site: pyrrolidone carboxylc acid (Gln) (in mature form from fc
F; 31/Modified site: amidated carboxyl end (Gly) (amide in mature form from fc
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C;Keywords:
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A; Residues: 1-91 <OKU>
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A; Contents: Brain
A; Contents: JC7393
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Best Local S
Matches 7
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C;Comment: This protein plays the
                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A21114
R;Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivier, R;Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivier, R;Sherwood, N.; Eiden, L.; Brownstein, 1983
Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983
A;Title: Characterization of a teleost gonadotropin-releasing A;Reference number: A21114; MUID:83195140
A;Accession: A21114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gonadoliberin - chum salmon
C;Species: Oncorhynchus keta (chum salmon)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 18-Jun-1993
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A; Status: preliminary
A; Molecule type: protein
A: Mosidues: 1-10 <SHE>
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A; Residues: 1-10
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Best Local :
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Best Local S
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gonadotropin-releasing hormone - cherry salmon C;Specles: Oncorhynchus masou (cherry salmon) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Aug-1997 C;Accession: I51180 R;Suzuki, M.; Hyodo, S.; Kobayashi, M.; Aida, K.; Urano, A. J. MOl. Endocrinol. 9, 73-82, 1992 A;Title: Characterization and localization of mRNA encoding the salmon-type gonadotrophi A;Reference number: I51180; MUID:92384893 A;Accession: I51180
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C;Species: Oncorhynchus tschawytscha (chinook salmon)
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C;Accession: I51092
R;Klungland, H.; Lorens, J.B.; Andersen, O.; Kisen, G.O.; Alestrom, P.
Moi. Cell. Endocrinol. 84, 167-174, 1992
A;Title: The Atlantic salmon prepro-gonadotropin releasing hormone gene and mRNA.
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Query Match
Best Local Similarity
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MOD_RES
NON_TER
SEQUENCE
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
PROGONADOLIBERIN GRELEASING HORMONE I) (GONADOTROPIN RELEASING
LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING
HORMONE I) (GNRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE I]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GON1_MESAU
009163;
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                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jansen H.T., Stevens P.J., Zeitler P., Lehman M.N.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT ST.
THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNRH1 OR GNRH OR LHRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                            EMBL; U91938; AAB51302.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                              Cleavage
                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                Pfam; PF00446; GnRH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT)
                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE GNRH FAMILY.
                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                PS00473;
                                                                                                                                                                                                                                                                                                                                                                   IPR002012; -.
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61
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Pred. No.
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PYRROLIDONE CARBOXYLIC ACID.

AMIDATION (G-11 PROVIDE AMIDE GROUP).
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                                                                                                                                                                                              APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
                                                                                                                                                                                                              GNRH-ASSOCIATED PEPTIDE SIMILARITY).
         Score
Pred.
                                                                                                                                                           PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                               GONADOLIBERIN
                                                                                                                                             SIMILARITY)
                                                                                                                                                                             ACTIVITY
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                                                                         FC94995676F77180
                                                                                                                              AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                            SIMILARITY).
         NO;
                                                                                                                                                                                                                                                                                                                       Hormone;
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0.00038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                             (BY SIMILARITY
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                                                                                                                                (G-11)
                           DB 1;
          .00039
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                                                                                                                                                                                                                                                                                                                         Amidation; Hypothalamus;
                                                                                                                                  PROVIDE
                         Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
; Cricetinae;
                                                                                                                                                                    ACID
                                                                                                                                  AMIDE GROUP)
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GON1_MACMU
ID GON1_PACCO
GON1_PACCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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Matches 9
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01-OCT-1996
01-OCT-1996
30-MAY-2000
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOTROPIN RELEASING LUTELNIZING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GONRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE I]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNRH1 OR GNRH OR LHRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GON1_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuroendocrinology 60:346-359(1994).
-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT STIMULATES
-i- EURCTION OF BOTH LUTBINIZING AND FOLLICLE-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Hypothalamus;
MEDLINE-95124501; PubMed-7545971;
Ma Y.J. (Osta M.E., Ojeda S.R.;
"Developmental expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9544;
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                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor alpha and its receptor in
                                                                                                                                                                                                                                                                                                         Signal.
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SEQUENCE
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EHWSYGLRPG 10
                                                                                                                                                                                                                                                                                                                                                                                                 S75918; AAB33096.1;
                                                                                                                                                                                                                                                                                                                                                                       PF00446;
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                                               Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                        PS00473;
                                                                                                                                                                                                                                                                                                                                                                     IPR002012; -. 0446; GnRH; 1.
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                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                       GNRH;
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7573
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96
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ACTIVITY (BY SIMILARITY).
ACTIVITY (BY SIMILARITY).
PYROLIDONE CARBOXYLIC AC
SIMILARITY).
AMIDATION (G-16 PROVIDE A
SIMILARITY).
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                                                  Score 60; DB 1;
Pred. No. 0.00042;
1; Mismatches 0
                                                                                                                                                                                                                                                GNRH-ASSOCIATED PEPTIDE
                                                                                                                              505394DAA261A3F2
                                                                                                                                                                                                                                                                    GONADOLIBERIN I
                                                                                                                                                                                                                                                                                 PROGONADOLIBERIN
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                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                                                                                                                                                                                                                              Hormone;
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i; Cercopithecidae
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                                                                                                                                                                                                                                                                                                                                                Amidation; Hypothalamus;
                                                                                  Length 67;
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                                                          Indels
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                                                                                                                                                                                                                ACID
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                                                                                                                                                                                 AMIDE GROUP) (BY
                                                                                                                                                                                                                                           BIOLOGICAL
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QHWSYGLRPG

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                    01-JAN-1990 (Rel. : 01-JAN-1990 (Rel. : 30-MAY-2000 (Rel. : PROGONADOLIBERIN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P45656;
01-NOV-1995
01-NOV-1995
30-MAY-2000
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                                                                                GON1_MOUSE
P13562;
01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94165563; PubMed-8137750;
Hayes W.P., Wray S., Battey J.F.;
"The frog gonadotropin-releasing hormone-I (GnRH-I) gene has
mammalian-like expression pattern and conserved domains in
GnRH-associated peptide, but brain onset is delayed until
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GONADOLIBERIN I PRECURSOR (GONADOTROPIN-RELEASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GnRH-associated peptide,
metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GON1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LH-RH) (LULIBERIN I).
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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(LUTEINIZING
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           13, Created)
13, Last sequence update)
39, Last annotation update)
1 PRECURSOR [CONTAINS: GONADOLIBERIN I
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Pred. No. 0.00056,
1; Mismatches (
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AMIDATION (G-34 PROVIDE AMIDE GROUP).
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HORMONE I) (GONADOTROPIN
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P49921;
                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation: GONADOLIBERIN I (LHRH I)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
(LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE I].
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phillips H.S., Nikolics K., Seeburg P.H.;
"A deletion truncating the gonadotropin-releasing responsible for hypogonadism in the hpg mouse.";
Science 234:1366-1371(1986).
"HE SECRETION OF BOTH LUTEINIZING AND FOLLICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M14872; Ar
MGD; MGI:95789;
                                                        Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                GNRH1 OR GNRH
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Mammalia; Eutheria;
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           SEQUENCE FROM N.A.
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TISSUE=Hypothalamus
                                              Mammalia; Eutheria;
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9; Conserv
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Metazoa; Rodentia; S
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                                              Cetartiodactyla;
                                                         Chordata; Craniata; Vertebrata;
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90.0%;
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PROLACTIN RELEASE-INHIBITING
APPEARS TO BE ESSENTIAL FOR I
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1C0766FA4826E4D9
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Sciurognathi;
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                                               Suina; Suidae;
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D9 CRC64;
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Baba Y., Matsuo H., Schally A.V.;
"Structure of the porcine LH- and FSH-releasing Confirmation of the proposed structure by conven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-72065376; PubMed-4942726;
Matsuo H., Arimura A., Nair R.M.G
"Synthesis of the porcine LH- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 44:459-463(1971).
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P01148;
P01148;
P01148;
P01148;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1988 (Rel. 07, Last sequence update)
01-APR-1988 (Rel. 07, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOTROPIN RELEASING (LUTEINIZING HORNONE RELEASING HORNONE I) (GONADORELIN); GNRH-ASSOCIATED
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MOD_RES
SEQUENCE
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MEDLINE=72117544; PubMed=4946275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the tryptophan residue in porcine LH and FSH-releasing horn chem. Biophys. Res. Commun. 45:483-487(1971). FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT STIME SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING
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0446; GnRH; 1.
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EMBL/GenBank/DDBJ databases
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GONADOLIBERIN I.
GONADOLIBERIN I.
GNRH-ASSOCIATED PEPTIDE I.
APPEARS TO BE ESSENTIAL FOR B
ACTIVITY.
PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-34 PROVIDE AMIDE
AMIDATION (G-34 PROVIDE AMIDE
); 8340474F32DDAA99 CRC64;
                                                                                                                                                                                                                         Score 60; DB pred. No. 0.00
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8340474F32DDAA99
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                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothalamus;
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                                                                                                                                                                                                                                                                                                                                             BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration
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                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in
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MEDILINE=86094338; PubMed=2867548; MEDILINE=86094338; PubMed=2867548; Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.; Adelman J.P., Mason A.J., Hayflick J.S., Mason A.J., Hayflick J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE I].
GNRH1 OR GNRH OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89366682; PubMed-2671939;
Hayflick J.S., Adelman J.P., Seeburg
"The complete nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adelman J.P., Mason A.J., Hayfilck J.S.
"Isolation of the gene and hypothalami
of gonadotropin-releasing hormone and
factor in human and rat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=89366682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biosynthesized in the human placenta.";
Biochem. Biophys. Res. Commun. 109:1061-1071(1982).
-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT ST.
THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of cDNA releasing hormone.";
Nature 311:666-668(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seeburg P.H., Adelman J.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=85012739; PubMed=6090951;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute.
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                  MOD_RES
MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
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                                                                                                                 CHAIN
PEPTIDE
PEPTIDE
                                                                                                                                                                                                                                                                                              MIM;
                                                                                                                                                                                                                 Cleavage
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                                                                                                                                                                                                Placenta;
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    SEQUENCE
                                                                                                                                                                              SIGNAL
                                                                                                 ACT_SITE
                                                                                                                                                                                                                                                                                                                                     WBL; M12578; AAA35916.1; -
WBL; M12578; AAA35916.1; -
WBL; X15215; CAA33285.1; -
R; A01410; RHHUG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE GNRH
                                                                                                                                                                                                                                                                                                        ; A01410; RHHUG.
; A26173; A26173.
; S05308; S05308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUTREPULSE OR LUTRELEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L., Rousseau P.;
chemical identity of the immunoreactive
                                                                                                                                                                                                                                                                                                152760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in
                                                                                                                                                                                                ps00473; GNRH; 1
on pair of basic
; pharmaceutical;
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      92
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Primates;
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          WW.
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                                                                                                                                                                                                                       residues; Hormone; Amidation;
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                                                                                                     GONADOLIBERIN I.
GNRH-ASSOCIATED F
APPEARS TO BE ESS
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        AMIDATION (G-34 PI
W -> S (IN REF. 3)
30A72221B076FA79
                                                                  ACTIVITY.

PYRROLIDONE CARBOXYLIC
                                                                                                                                                                 PROGONADOLIBERIN
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                                                                                                           ESSENTIAL
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                  CRC64
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                                                       AMIDE GROUP).
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                                                                                                                                                                                                                               Hypothalamus;
                                                                                                                 BIOLOGICAL
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Best Local
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                                                                                                                                                                                  DNA locu
Science
-I- FUNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-86094338; PubMed-2867548; Adelman J.P., Mason A.J., Hayfilck J.S., Seeburg P.H.; Adelman J.P., Mason A.J., Hayfilck J.S., Seeburg P.H.; of gonadotropin-releasing hormone and prolactin release-inhibiting factor in human and rat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
(LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GON1_RAT P07490;
                       This SWISS-PROT entry is copyright. It is produced through a collaboration-between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                Maier C.C., Marchetti B., Leboeuf R.D., Blalock J.E.; "Thymocytes express a mRNA that is identical to hypothalamic luteinizing hormone-releasing hormone mRNA."; Cell. Mol. Neurobiol. 12:447-454(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-89384661; PubMed-2476669;
Bond C.T., Hayflick J.S., Seeburg P.H., ,
"The rat gonadotropin releasing hormone:
                                                                                                                                                                                                                                MEDLINE-87149087; PubMed-3547652; Adelman J.P., Bond C.T., Douglass
                                                                                                                                                                                                                                                                                                                                               TISSUE-Thymus;
MEDLINE-93105480; PubMed-1468115;
                                                                                                                               -!- SIMILARITY:
                                                                                                                                                                                                                                                                         SEQUENCE OF 1-47 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 hypothalamic expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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                                                                                                                            TISSUE SPECIFICITY: CENTRAL NERVOUS SIMILARITY: BELONGS TO THE GNRH FAMI
                                                                                                                                                                                  FUNCTION:
                                                                                                                                                                                                           Locus."
                                                                                                                                                        HORMONES
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                                                                                                                                                                                                                     mammalian genes transcribed
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                                                                                                                                                                   STIMULATES THE SECRETION OF GONADOTROPINS; IT ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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    (LULIBERIN I);

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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
96
                                                                                                                                                                                                                                  T., Douglass
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Pred.
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Sciurognathi; Muridae;
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                                                                                                                             GNRH FAMILY.
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0.00057;
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locus: structure
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; Murinae; Rattus.
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Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                _TUPGB
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PEPTIDE
ACT_SITE
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PIR;
                                                                                              This SWI
                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
(LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE I].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
                                         use by non-profit institutions as long as modified and this statement is not removed. Use entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        TISSUE-Hypothalamus;
MEDLINE-97079639; PubMed-8921350;
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                         GON1_TUPGB
Q95335;
                                                                                     the
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                GNRH1 OR GNRH
                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00446;
                    EMBL; U63326; AAB16837.1;
                                                                                                                                                                                                                    Fernald R.D.;
                                                                                                                                                                                                                                Kasten
                                                                                                                                                                                                                                                                                                                   Tupaia glis belangeri (Common tree shrew)
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           InterPro
                                                                                                                                                                                                           "Characterization of two new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EHWSYGLRPG
                                                                                   s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                 SIMILARITY:
                                                                                                                                                                FUNCTION: STIMULATES THE
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                                                                                                                                                                                                direct evidence
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Similarity 90.0%;
9; Conservative
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                                                                                                                                                                                                                              L., White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002012;
                                                                                                                                                                          Endocrinol. 104:7-19(1996)
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Scandentia; Tupaiidae; Tupaia.
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mesencephalic GnRH c
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PYRROLIDONE CARBOXYLIC ACID
AMIDATION (G-34 PROVIDE AMI
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GONADOLIBERIN I.
PROLACTIN RELEASE-INHIBITING
APPEARS TO BE ESSENTIAL FOR E
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                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                               Bond C.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                     92
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                                                                                                                                                    GONADOTROPINS; IT STIMULATES FOLLICLE-STIMULATING
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                                                                          its content
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                                                                                                                                                                                               the tree shrew: expression in
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BIOLOGICAL
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p37041; P20407;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last anotation update)
GONADOLLBERIN I (GONADOTROPIN-RELEASING HORMO
CLULIBERIN I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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i_CHICK
GON1_CHICK
P37042; P20407;
01-FEB-1991 (Rel
                                                                                                                                                                                                   Alligator mississippiensis (American alligator).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Crocodylidae; Alligatorinae; Alligator
                                                                                                                                      Hormone;
MOD_RES
MOD_RES
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                                                                                                                                                                                                                                                                                  NCBI_TaxID=8496;
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InterPro; IPR002012;
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QHWSYGLQPG
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9; Conserv
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rE; PS00473; GNRH; 1
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on pair of
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8; Conserv
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n pair of bac'
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                  STANDARD;
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                                                                                                 88.9%;
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                                                                                         ; Score 56; DB
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2; Mismatches
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GNRH-ASSOCIATED PEPTIDE
APPEARS TO BE ESSENTIAL
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PYRROLIDONE CARBOXYLIC
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4FDBF2C58CF5F63B CRC64;
                                                                                                                                PYRROLIDONE CARBOXYLIC AMIDATION. 284B23D7286B45A3 CRC64;
                     PRT;
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    I) (GNRH-I) (LH-RH

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30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOTROPIN RELEASING
(LUTETRIZING HORMONE RELEASING HORMONE I) (GONADOTROPIDE I).
HORMONE I) (GNRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE I).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
STRAIN-WHITE LEGHORN;
STRAIN-HOLLINE=9405935; PubMed=7902095;
Dunn I.C., Chen Y., Hook C., Sharp P.J., Sang H.M.;
"Characterization of the chicken preprogonadotrophin-releasing "Characterization of the chicken preprogonadotrophin-releasing hormone-I gene:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Hypothalamus;
MEDLINE-82265778; PubMed=7050119;
King J.A., Millar R.P.;
Ring J.A., Millar R.P.;
Rinceture of chicken hypothalamic luteinizing hormone. II. Isolation and characterization.";
J. Biol. Chem. 257:10729-10732(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITME-82265777; PubMed=/0304140, MEDITME-82265777; PubMed=/0304140, King J.A., Millar R.P.; King J.A., Millar R.P.; "Structure of chicken hypothalamic luteinizing hormone-releasing "Structure of chicken hypothalamic non partially purified".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 24-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is no modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Hypothalamus;
King J.A., Millar R.P.;
"Structure of avian hypothalamic
S. Afr. J. Sci. 78:124-125(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNTHESIS
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                                                                                                                 CHAIN
PEPTIDE
PEPTIDE
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 257:10722-10728(1982).
-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS
-i- SIMILARITY: BELONGS TO THE GNRH FAMILY.
                                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                              or send an
                                                                                                                                                                                                                                                                                                                                                               entities requires a
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SIGNAL
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                                                                                                                                                                                                                                                                                                      X69491; CAA49246.1;
S33507; S33507.
              EHWSYGLRPG
                                                                                                                                                                                                                                                                        PF00446;
Similarity
8; Conser
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                                                                                                                                                                                                                                                          PS00473; GNRH;
                                                                                                                                                                                                                                                                        IPR002012; -. 0446; GnRH; 1.
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                                               Score 56; DB pred. No. 0.00 2; Mismatches
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                                                                                                                      PROGONADOLIBERIN I.
GONADOLIBERIN I.
GONAH-ASSOCIATED PEPTIDE I.
PYRROLIDONE CARBOYYLIC ACID.
AMIDATION (G-34 PROVIDE AMIDE GROUP).
61AEB7EBAF508B6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gonadotrophin-releasing hormone.";
                                                                                                                                                                                                                                                  Hormone; Amidation; Hypothalamus;
                                                                  .0029;
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                                                     Indels
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OHMSYGLOPG

JLT 12 L_HAPBU GON1_HAPBU

STANDARD;

PRT;

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Actinopterygii; Neopterygii; Teleostei; Eutel Acanthomorpha; Acanthopterygii; Percomorpha; Cichlidae; Astatotilapia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GONADOLIBERIN I PRECUSOR (GONADOTROPIN-RELEASING HORMONE I) (GNRH-I)
(LH-RH I) (LULIBERIN I).
 PEPTIDE PEPTIDE MOD_RES
                                                      Signal;
SIGNAL
                                                                                                                                                                           the European Bioinformatics Institute. The by non-profit institutions as low modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                          and pumpkinseed fish.";
Regul. Pept. 57:43-53(1995)
-!- FUNCTION: STIMULATES TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haplochromis burtoni.
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P51918; 093387;
01-OCT-1996 (Re
                                                                                                                      EMBL; U31865; AAC59691.1; -. EMBL; AF076961; AAC27716.1; -. InterPro; IPR002012; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White S.A., Kasten T.L., Bond C.T., Adelman J.P., "Three gonadotropin-releasing hormone genes in on novel roles for an ancient peptide.";

Proc. Natl. Acad. Sci. U.S.A. 92:8363-8367(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-95396797; PubMed-7667296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pituitary;
MEDLINE-95372591; PubMed-7644702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Ontogeny of gonadotropin-releasing hormone (GnRH) gene expression reveals a distinct origin for GnRH-containing neurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-99061842;
                                                                                 PROSITE; PS00473; GNRH; 1.
Cleavage on pair of basic
                                                                                                            Pfam; PF00446; GnRH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sherwood N.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        White S.A., Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White R.B., Fernald R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-8153;
                                                                                                                                                                                                                                                                                                                                                                                                                Primary structure of solitary form of gonadotropin-releasing hormone (GnRH) in cichlid pituitary; three forms of GnRH in brain of cichlid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Powell J.F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF
                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE GNRH FAMILY.
                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: SYNTHESIZED IN PREOPTIC NEURONS AND I TRANSPORTED TO THE PITUITARY IN THE PREOPTIC-HYPOPHYSEAL MASS SPECTROMETRY: MW-1113.9; METHOD-MALDI; RANGE-23-32.
                                                                                                                                                                                                                                                                                                                                  GONADAL AXIS.
TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                           RESPONSIBLE FOR THE
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                                                                    Multigene
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    23632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9843638;
                                                                    family.
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                                                                                                                                                                                                                                                                                                                                                             REGULATION
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                                                                                   residues;
GONADOLIBERIN I.
GNRH-ASSOCIATED PEPTIDE
PYRROLIDONE CARBOXYLIC A
                                         PROGONADOLIBERIN
                                                                                 Hormone;
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                                                                                                                                                                                                         Usage
                                                                                 Amidation; Hypothalamus;
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Warby C
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               (POTENTIAL)
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MBL outstation -
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P70074;
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
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Submitted (SEP-1996) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GONADOLIBERIN I PRECURSOR (GONADOTROPIN-RELEASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGMA
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SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
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61E79C990328D73E CRC64;
                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC SIMILARITY).
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GNRH-ASSOCIATED PEPTIDE
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Eutele Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neote Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Sparidae; Sparus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GONADOLIBERIN I PRECURSOR (GONADOTROPIN-RELEASING HORMONE I) (GNRH-I)
(LH-RH I) (LULIBERIN I) (SBGNRH).
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01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Powell J.F.F., Zohar Y., Elizur A., Park M., Fischer W.H., Craig A.G., Rivier J.E., Lovejoy D.A., Sherwood N.M.; Three forms of gonadotropin-releasing hormone characterized brains of one species."; J. S.A. 91:12081-12085(1994).

Proc. Natl. Acad. Sci. U.S.A. 91:12081-12085(1994).

-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.

-i- MASS SPECTROMETRY: MW-1113.6; METHOD-MALDI; RANGE-26-35.

-i- SIMILARITY: BELONGS TO THE GURH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDITINE-95268499; PubMed=7749463; Gothilf Y., Elizur A., Chow M., Chen T.T., Zohar Y.; "Molecular cloning and characterization of a novel gonadotropin-releasing hormone from the gilthead seabream (Sparus aurata)."; mol. mar. Biol. Biotechnol. 4:27-35(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sparidae; Sparus.
NCBI_TaxID=8175;
  GON1_CAVPO
054713;
15-DEC-1998
15-DEC-1998
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1; Mismato
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GONADOLIBERIN I.
GONAH-ASSOCIATED PEPTIDE I (POTENTIAL:
PYRROLIDOME CARBOXYLIC ACID.
AMIDATION (G-36 PROVIDE AMIDE GROUP)
49313FD6FD6B87DA CRC64;
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PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
(LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING
HORMONE I) (GNRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE I].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNRH1 OR GNRH OR LHRH
                                                                                                                                                                                                                                        Placenta;
SIGNAL
                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reveals a unique decapeptide and existence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97462693; PubMed=9322920;
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STRAIN-HARTLEY WHITE; TISSUE-Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10141;
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QYWSYGVRPG
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GNRH-ASSOCIATED PEPTIDE I.
APPEARS TO BE ESSENTIAL FOR
ACTIVITY (BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleosto
Hystricognathi; Caviidae; Cavia.
                                                  Score 51; DB 1;
Pred. No. 0.022;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  King
                                                                                                                            SIMILARITY)
                                                                                                                                           AMIDATION
                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                PROGONADOLIBERIN I.
                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                  ACF74613F456D663 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.C.;
                                                                                                                                                                                                                                                                    Hormone; Amidation; Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND
AND
                                                                                                                                                                                                                                                                                                                                           noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                      There are no restrictions ong as its content is in
                                                                                                                                           (G-34 PROVIDE AMIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GONADOTROPINS; IT STIMULATES FOLLICLE-STIMULATING
                                                      0;
                                                                              Length 92;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                               BIOLOGICAL
                                                                                                                                               GROUP) (BY
                                                         0;
                                                         Gaps
                                                            0
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THIS PAGE BLANK (USPTO)

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
   SPTREMBL_16:*

1: Sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_unclassific
13: sp_vertebrate:
14: sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           November 13, 2001, 14:26:54; Search time 46.47 Seconds (without alignments) 28.471 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                            425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-412-558-1
63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
sp_organelle:*
sp_phage:*
sp_rodent:*
sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHWSYGLRPG 10
                                                                                                                        sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                             425026
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | ဖ | 8 | 7 | 0 | ഗ | 4 | ω | 2 | 1 | Result No. |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------|
| 47 | 47 | 47 | 47 | 47 | 47 | 47 | 47 | 47 | 47 | 47 | 47 | 49 | 50 | 52 | 54 | 54 | 54 | 60 | Score |
| 74.6 | 74.6 | 74.6 | 74.6 | 74.6 | 74.6 | 74.6 | 74.6 | 74.6 | 74.6 | 74.6 | 74.6 | 77.8 | 79.4 | 82.5 | 85.7 | 85.7 | 85.7 | 95.2 | Query Match |
| 94 | 94 | 90 | 90 | 88 | 82 | 82 | 82 | 82 | 33 | 33 | 10 | 10 | 91 | 90 | 99 | 95 | 87 | 91 | Length |
| 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | μ W | 13 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | DB. |
| Q9DEH5 | Q9DEH6 | Q9DD49 | Q9IA09 | Q9PSY9 | Q918P9 | 091800 | Q9W7G1 | Q92094 | Q9PT34 | Q9W7G0 | P81751 | P81749 | Q9DGC8 | Q9IAU2 | Q9IA10 | 073812 | Q9YI26 | Q9PRH0 | ID |
| Q9deh5 carassius a | Q9deh6 carassius a | Q9dd49 oryzias lat | Q9ia09 dicentrarch | Q9psy9 sparus aura | Q9i8p9 oncorhynchu | Q918q0 oncorhynchu | Q9w7g1 oncorhynchu | Q92094 oncorhynchu | Q9pt34 oncorhynchu | Q9w7g0 oncorhynchu | P81751 clupea pall | P81749 clupea pall | oryzia | Q9iau2 rana dybows | Q9ia10 dicentrarch | O73812 morone saxa | Q9yi26 sparus aura | Q9prh0 anguilla ja | Description |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | <u>ω</u> | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-----------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 39 | 39 | 39 | 39 | 39 | 40 | 40 | 40 | 41 | 41 | 41 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 47 |
| 61.9 | 61.9 | 61.9 | 61.9 | 61.9 | 63.5 | 63.5 | 63.5 | 65.1 | 65.1 | 65.1 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 74.6 |
| 417 | 388 | 379 | 322 | 101 | 1000 | 565 | 283 | 532 | 316 | 315 | 828 | 686 | 114 | 107 | 93 | 87 | 86 | 86 | 86 | 85 | 85 | 80 | 75 | 10 | 94 |
| ഗ | _ | 10 | N | œ | N | N | N | v | 11 | ഗ | 10 | 4 | 6 | σ | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 6 | 13 | 13 |
| Q9TXI2 | Q9YD14 | Q9LV12 | Q9F3C9 | 079746 | Q9PCD0 | Q9KM11 | Q9F2U4 | 044866 | 008782 | P91045 | Q9SZR5 | Q9H6R3 | 097655 | Q9TSI3 | Q9DG36 | Q9PRI3 | Q9PT25 | Q9PW69 | 042471 | Q9IA08 | 073811 | Q9DGC9 | Q9TTVO | P81750 | Q9DDD8 |
| Q9txi2 caenorhabdi | Q9yd14 aeropyrum p | Q91v12 arabidopsis | Q9f3c9 streptomyce | 079746 omanosaura | 09pcd0 xylella fas | Q9km11 vibrio chol | Q9f2u4 streptomyce | O44866 caenorhabdi | | P91045 caenorhabdi | Q9szr5 arabidopsis | Q9h6r3 homo sapien | 097655 macaca mula | Q9tsi3 macaca mula | rana cate | Q9pri3 anguilla ja | | Q9pw69 typhlonecte | O42471 carassius a | Q9ia08 dicentrarch | 073811 morone saxa | Q9dgc9 oryzias lat | Q9ttv0 trichosurus | P81750 clupea pall | Q9ddd8 brachydanio |

ALIGNMENTS

| S T T T K C C C C C C C C C C C C C C C C | RESU Q9PF |
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RESULT

O738112

O738112

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O778
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Best Local S
Matches
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Best Local S
Matches 8
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TREMBLREL. 16, Last annotation update)
GONADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
(LULIBERIN) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sparus aurata (Gilthead sea bream).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostel;
Acanthomorpha; Acanthopterygii; Percomor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9YI26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sparidae; Sparus.
NCBI_TaxID=8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nabissi M.;
Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -73812 PRELIMINARY; PRT; 95 AA.

073812;
073812;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MG-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
001-MAR-2001 (TrEMBLREL. 16, Last annotation update)
001-MAR-2001 (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Ćraniata; Actinopterygii; Neopterygii; Teleostei; Acanthomorpha; Acanthopterygii; Percomor Moronidae; Morone.
NCBI_TaxID=34816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amidation; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
SEQUENCE FROM N.A.
Chow M.M., Kight K.E., Gothilf Y., Alok D., Zohar Chow M.M., Kight K.E., Gothilf Y., Alok D., Zohar Submitted (MAR-1998) to the EMBL/GenBank/DDBJ date Submitted (MAR-1998) THE SECRETION OF GONADOTF -- FUNCTION: STIMULATES THE SECRETION OF GONADOTF -- SIMILARITY: TO THE GNRH FAMILY.
EMBL; AF056314; AAD03817.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                        Morone saxatilis (Striped bass).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LULIBERIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>س</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS. SIMILARITY: TO THE GNRH FAMILY.

L; AF046801; AAD02427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||||||||||
QHWSYGLRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EHWSYGLRPG
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00446; GnRH;
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8; Conser
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87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
9871 MW;
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:leostei; Euteleostei; Neoteleostei;
Percomorpha; Perciformes; Percoide
                                                                                                                                                                                                                                                                                                                                   Percomorpha;
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No. 0.0029;
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0.031;
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                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostom1;
Euteleostei; Neoteleostei;
rpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                               ODBJ databases
GONADOTROPINS
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DR
DR
KW
SQ
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Best Local S
Matches 8
                                                                                                          RESULT
Q9IAU2
                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                   Qy
SSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; TPR002012;
pfam; PF00446; GnRH; 1
pROSITE; PS00473; GNRR
Amidation; Hormone.
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9IA10
Q9IA10;
01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00NADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dicentrarchus labrax (European sea bass).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gonzalez-Martinez D., Madigou T., Zmora N., Anglade I., Zohar Y., Elizur A., Munoz Cueto J.A., Kah O.; Zohar Y., Elizur A., Munoz Cueto J.A., Kah O.; Zohar Y., Elizur A., Munoz Cueto J.A., Kah O.; Gonzalez Charles and J. Martinez Constant Preparation of three different prepro-GnRH "Gonzalez Charles In the brai European sea bass (Dicentrarchus labrax)."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=13489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moronidae; Dicentrarchus
Q9IAU2;
Q9IAU2;
01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                              Amidation;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).

-!- SIMILARITY: TO THE GNRH
EMBL; AF224279; AAF62898.1;
Interpro; IPR002012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zmora N., Zohar Y., Elizur A.,
Zmora N., Zohar Y., Elizur A.,
"3 GnRH form in the seabass Di
"3 GnRH form in the seabass Di
Submitted (JAN-2000) to the EM
-j- FUNCTION: STIMULATES THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00473; GNRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPROUZULZ;
Pfam; PF00446; GnRH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: STIMULATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                     1 EHWSYGLRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QHWSYGLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHWSYGLRPG
                                                                                                                                        G
                                                                                                                                                                                                         QHWSYGLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
                                                                                                                                                                                                                                                                                              h 85.7%;
Similarity 80.0%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hormone.
95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone.
99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
(TrEMBLrel. (TrEMBLrel.
                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNRH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10411
                                                                                                                                                                                                                                                                                                                                                                                                                        10758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%;
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       15,
15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 13 pred. No. 0.034; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dicentrarchus labrax.";
EMBL/GenBank/DDBJ databases
E SECRETION OF GONADOTROPINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     980C6988FC279BFC
         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                              Score 54; DB 13
Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                          EC8AEEC93CC02904 CRC64;
                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                        90
                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GONADOTROPINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 95;
                                                                                                                                                                                                                                                                                                                                                             Length 99;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY
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                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT DESCRIPTION OF STATE OF
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                                                                          В
    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 8
                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                        Biochem. Biophys.
EMBL; ABO41333; BA
CHAIN 22
SEQUENCE 91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDGNRH.
Oryzias latipes (Medaka fish).
Oryzias, Metazoa; Chordata; Craniata; Vertebrata; Euteleos Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
NCBI_TaxID=8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF139911; AAF44343.1; InterPro; IPR001211; -. InterPro; IPR002012; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PREPRO-GONADOTROPIN-RELEASING HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of a Novel Gonadotropin-Releasing Mol. Cell. Endocrinol. 0:0-0(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; (
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed-11006121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9DGC8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9DGC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000303; -; 1. PROSITE; PS00473; GNRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kwon H.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoo M.S., Kang H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana dybowskii (Frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GONADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LULIBERIN)
                                                                                                                                                                                                                                                                                                                                                                                      .atipes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                          22
                                                                                                   1 EHWSYGLRPG 10 : | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                            Novel Form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EHWSYGLRPG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: STIMULATES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QHWSFGLSPG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 80.
8; Conservative
                                                                                                                                                                   Similarity 70.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Amano M., Yoshiura Y., Suetake H.,
Form of Gonadotropin-Releasing Horm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                    s. Res. Commu
BAB16303.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO THE GNRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10368 MW;
                                                                                                                                                                                                                                                                                          10307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Distribution and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choi H.S., Chun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anura;
                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                           Commun.
                                                                                                                                                                                            . 0%;
                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB
Pred. No. 0.07
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a; Craniata; V
Neobatrachia;
                                                                                                                                                                   Score 50; DB 13
Pred. No. 0.16;
2; Mismatches
                                                                                                                                                                                                                                                                                        GONADOTROPIN-RELEASING HORMONE A00F2BED6FD6E0B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECRETION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C3D573E78B52ABFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                             276:298-303(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hormone([Trp8]GnRH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phamacological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.Y.,
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0.071;
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a; Ranoidea;
                                                                                                                                                                                                                  DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Aida K.;
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Neoteleostei;
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Ranidae; Rana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Millar R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                            Medaka,
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P 1749
P 181749
P 181
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Query Match
Best Local
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MOD_RES
MOD_RES
SEQUENCE
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MEDLINE-2011/4351; PubMed-10650929;
Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.
Chang J.P., Rivier J.E., Sherwood N.M.;
"Primary structure and function of three gonadotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P81749 PRELIMINARY; PRT; 10 AA.
P81749;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GONADOLLBERIN I (GONADOTROPIN-RELEASING HORMONE I) (GNRH-I)
                                                                                                                                                                                                                                                                                                                                                                            P81751 PRELIMINARY; PRT; 10 AA.
P81751;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GONADOLIBERIN III (GONADOTROPIN-RELEASING HORMONE III)
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Clupeinae; Clupea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinopterygii; Neopterygii; Teleostei; Clupeinae; Clupea.
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Clupea pallasii (Pacific herring).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
 SEQUENCE
                 Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1
Hormone; Amidation; Hypotl
                                                                                                                                                                                                                                                                            NCBI_TaxID=30724;
                                                                                                                                                                                                                                                                                                                                               Clupea pallasii (Pacific herring).
                                                                                                                                                                                                                                                                                                                                                                RH III) (LULIBERIN III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002012; -. Pfam; PF00446; GnRH; 1. PROSITE; PS00473; GNRH; 1.
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               Amidation;
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 1230 MW; 284E
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70.0%;
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                                                                                                                                                                                                                                                                                                           ; Craniata;
; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.
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284B20B72871F5A3
 284B3233786B45A3 CRC64;
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                                                                                                                                                                                                                                                                                                              Vertebrata; E Clupeomorpha;
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a; Clupeidae;
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RESULT Q9PT34 ID 95 AC 97 AC 9
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Q9W7G0
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Matches 7
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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SEQUENCE FROM N.A.
MEDLINE=99312119; PubMed=10385393;
Won Schalburg K.R., Sherwood N.M.;
Von Schalburg the following the fo
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SEQUENCE
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                                                                                                                                                                                                             O9PT34 PRELIMINARY; PALL OPPT34; O9PT34; O1-MAY-2000 (TrEMBLrel. 13, Created) O1-MAY-2000 (TrEMBLrel. 13, Last sequence up O1-MAY-2001 (TrEMBLrel. 16, Last annotation GONADOLIBERIN (GONADOTROPIN-RELEASING HORMON (LULIBERIN) (FRAGMENT).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorh, NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amidation;
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33
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Pred. No. 0.18;
1; Mismatches
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n rainbow trout.";
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HORMONE) (GNRH)
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0.051;
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HORMONE) (GNRH) (LH-RH)
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                                                                                     Oncorhynchus
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                                                                                                                                                        Euteleostomi;
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RESULT
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-99312119; PubMed=10385393;
WON Schalburg K.R., Sherwood N.M.;
Von Schalburg K.R., Sherwood gonadotropin-releasing hormone
"Regulation and expression of gonadotropin-releasing hormone
differs in brain and gonads in rainbow trout.";
Endocrinology 140:3012-3024(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

von Schalburg K.R., Sherwood N.M.;

submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pfam; PF00446; GnRH; 1.
proDom; PD005116; -; 1.
pROSITE; PS00256; AKH; UNKNOWN_1.
pROSITE; PS00473; GNRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
-!- SIMILARITY: TO THE GNRH
EMBL; AF110533; AAD43461.1;
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Protacanthopterygii; Salmoniformes; Salm
NCBI_TaxID=8023;
                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
60NADOLIBERIN PRECURSOR (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002047;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.

TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                              (LULIBERIN)
                                                        PROSITE;
           SIGNAL
CHAIN
CHAIN
                                                                                        -i- EUNCTION: STIMULARIES 1
-i- SIMILARITY: TO THE GNU
-i- SIMILARITY: TO THE GNU
EMBL; D31868; BAA06666.1;
InterPro; IPR002012; -.
InterPro; IPR002047; -.
                                                                                                                                                                   "Two differing precursor genes
                                                                                                                                                                              Urano A.,
                                                                                                                                                                                        Ashihara M.,
                                                                                                                                                                                                 MEDLINE=96020547; PubMed=8546809;
                                                                                                                                            releasing hormone exist in salmo
J. Mol. Endocrinol. 15:1-9(1995)
                                                                               Pfam;
  SEQUENCE
                                            Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EHWSYGLRPG
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                                                                                                                                    FUNCTION: STIMULATES THE SECRETION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                   QHWSYGWLPG
                                                                               PF00446; GnRH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001152;
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                                                        PS00256; AKH; UNKNOWN_1.
PS00473; GNRH; 1.
                                                                                                                                                                              M., Suzuki M., Kubokawa K., Yoshiura
Aida K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hormone.
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                                               Hormone;
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                           Signal.
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33
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                                                                                                                          GNRH FAMILY
       M.
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1; Mismatches
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                                                                                                                                                             salmonids.";
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     GNRH-ASSOCIATED PEPTIDE. C64044EA521B2B8B CRC64;
                            GNRH
                                      POTENTIAL
                                                                                                                                                                        for the
                                                                                                                                                                                                                                                                Salmonidae; Oncorhynchus.
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                                                                                                                                                                        salmon-type
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                                                                                                                                                                                                                                                                        Vertebrata;
Euteleostei;
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                                                                                                                                          GONADOTROPINS
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                                                                                                                                                                           gonadotropin.
                                                                                                                                                                                                                                                                                     Euteleostomi;
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Best Local S
Matches 7
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Best Local Similarity
Matches 7; Conser
                                                                                                                                                            091800;
01-CCT-2000 (TrEMBLrel. 15, Cr
01-CCT-2000 (TrEMBLrel. 15, La
01-MAR-2001 (TrEMBLrel. 16, La
GONADOLIBERIN (GONADOTRODIN-Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Von Schalburg K.R., Sherwood N.M.; "Regulation and expression of gonadotropin-releasing differs in brain and gonads in rainbow trout."; Endocrinology 140:3012-3024(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99312119; PubMed-10385393;

Amaiburg K.R., Sherwood N.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID-8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GONADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
                                Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Actinopterygli; Meopterygli; Teleostei; Euteleostei; Protacanthopterygli; Salmoniformes; Salmonidae; Oncor NCBI_TaxID-8022;
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SEQUENCE
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PROSITE; PS00256; AKH; UNKNOWN_1
PROSITE; PS00473; GNRH; 1.
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                                                                                                                                                                                                                                                                                        091800
SEQUENCE FROM N.A
                                                                                                                                                     (LULIBERIN).
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                                                                                                                                                                   Last sequence update)
Last annotation update)
(-RELEASING HORMONE) (GNR
                                                                                                                                                                                                                                          Created)
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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No.
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0.47;
                                                                                    Vertebrata; Euteleostomi;
Euteleostei;
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                                                                Oncorhynchus
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RESULT
Q9PSY9
ID Q0
AC Q0
DT 01
DT 01
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Q918P9
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Best Local S
Matches 7
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Best Local :
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 01-MAY-2000
01-MAY-2000
01-MAR-2001
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Q918P9;
01-OCT-2000
01-OCT-2000
01-MAR-2001
                                Q9PSY9
                                                                                                                                                                                                                                                                           TISSUE-BRAIN; Ferriere F., Bailhache T., Jego P.; Ferriere F., Bailhache T., Jego P.; "Oncorhynchus mykiss sGnRH-II cDNA in the brain."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.-!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS
                                                                                                                                                                                                                                                                                                                                                  Oncorhynchus mykiss (Rainbow t
Bukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Protacanthopterygii; Salmonifc
NCBI_TaxID-8022;
                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation updat GONADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferriere F., Bailhache T., Jego P.;
"Oncorhynchus mykiss SGnRH-I cDNA from brain.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
-:- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS
SIMILARITY)
                                                                                                                                                                                         PROSITE; PS00473; GNRH;
Amidation; Hormone.
SEQUENCE 82 AA; 9203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00446; GnRH; 1.
PROSITE; PS00256; AKH; UNKNOWN_1.
PROSITE; PS00473; GNRH; 1.
Amidation; Hormone
                                                                                                                                                                                                                         InterPro; IPR002012;
Pfam; PF00446; GnRH;
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                                                                                                                                                                                                                                            SIMILARITY). TO THE GNRH EMBL; AF232213; AAF91281.1;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        (LULIBERIN).
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                                                                 15
                                                                                                                 1 EHWSYGLRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EHWSYGLRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QHWSYGWLPG
                                                                                              QHWSYGWLPG
                                                                                                                                      l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR00201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hormone.
82 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Tremblrel 15, (Tremblrel 15, 15)
 (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9198
                                                                                                                                                                                            9203 MW;
                                                                                                                                                 74.68;
70.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
70
                                                                                                                                                                                                                                                                                                                                                               Salmoniformes; Salmonidae; Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                       Created)
                                                                                                                                                                                                                                                         FAMILY.
Last sequence update)
Last annotation update)
                                                                                                                                      ۲.
                                                                                                                                                 Score 47; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       trout) (Salmo gairdneri); Craniata; Vertebrata; E
Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7595A0B896556A69 CRC64;
                                                                                                                                                                                           8053F4F221A0FF08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                tation update)
HORMONE) (GNR
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                                                                                                                                                  0.47;
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                                                                                                                                                            DB
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                                                                                                                                                                                                                                                                                                                                                                                                                  (GNRH)
                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                  (LH-RH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY
                                                                                                                                                                                                                                                                              (BY
                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                      0;
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Page 6

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Search completed: November 13, 2001, 14:34:00 Job time: 426 sec
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Submitted (Feb-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (Feb-1998) to the EMBL/GenBank/DDBJ databases.

SUBMITTER STIMULATES THE SECRETION OF GONADOTROPINS (BY SIMILARITY).

C SIMILARITY: TO THE GNRH FAMILY.

C -!- SIMILARITY: TO THE GNRH FAMILY.

C -!- SIMILARITY: TO THE GNRH FAMILY.

C -!- SIMILARITY: TO THE GNRH FAMILY.

REMBL; AF046799; AADD2425.1; -.

REMBL; AF0
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GONADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
(LULIBERIN) (FRAGMENT).
Sparus aurata (Gilthead sea bream).
Sparus aurata (Gilthead sea bream).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Sparidae; Sparus.
NCBI_TaxID=8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-OVARY;
                                                                                                                                                                                                     1 EHWSYGLRPG 10
:||||| ||
24 QHWSYGWLPG 33
                                                                                                                                                                                                                                                                                                                                                                                                                      74.6%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 13; Length 88; 
Pred. No. 0.51; 
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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